Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.

- If you encounter an accession number from an older search run against UniProt (results file extension **.rup)** that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

  http://www.pir.uniprot.org/database/archive.shtml

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

STIC-Biotech/ChemLib 160352

From: Swope, Sheridan
Sent: Monday, July 25, 2005 2:40 PM
To: STIC-Biotech/ChemLib
Subject: 10/726,967

CRF

For 10/726,967, pls search:
(A)--Claim 1(18)
SID 3: oligo search against the NT & AA data bases.

(B)
SID 52 against the NT & AA data bases.
For any hits that are 100% identical, pls align with:
residues 22-41 of SID 1,

If you have questions, pls ask me or David Schreiber.

Thanks

Sheridan Swope, Ph.D.
Patent Examiner, AU 1656
Recombinant Enzymes
571-272-0943 (voice)
E02B71 Remsen Bld (Office)
E03C70 Remsen Bld (Mailbox)

****
STAFF USE ONLY

Searcher:_____
Searcher Phone: 2-
Date Searcher Picked up:____
Date Completed:_____
Searcher Prep/Rev. Time:___
Online Time:_____

****
Type of Search

NA#:_____ AA#:_____
Interference:____ SPDI:___
S/L:_____ Oligomer:_____
Encode/Transl:_____
Structure#:_____ Text:___
Inventor:____ Litigation:___

****
Vendors and cost where applicable
STN:_____
DIALOG:_____
QUESTEL/ORBIT:_____
LEXIS/NEXIS:_____
SEQUENCE SYSTEM:_____
WWW/Internet:_____
Other(Specify):_____

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: July 26, 2005, 16:28:49 ; Search time 43 Seconds
(without alignments)
27.776 Million cell updates/sec

Title: US-10-726-967A-3
Perfect score: 16
Sequence: 1 TQHGIRLPLRSGLGGA 16

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 513545 seqs, 74649064 residues

Word size : 0

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	16	100.0	24	4	US-09-724-566A-47	Sequence 47, Appl
2	16	100.0	419	4	US-09-724-566A-57	Sequence 57, Appl
3	16	100.0	419	4	US-09-471-669A-57	Sequence 57, Appl
4	16	100.0	420	4	US-09-724-566A-60	Sequence 60, Appl
5	16	100.0	420	4	US-09-471-669A-60	Sequence 60, Appl
6	16	100.0	428	4	US-09-548-372D-51	Sequence 51, Appl
7	16	100.0	428	4	US-09-548-367D-51	Sequence 51, Appl
8	16	100.0	428	4	US-09-551-853D-51	Sequence 51, Appl
9	16	100.0	428	4	US-09-416-901B-51	Sequence 51, Appl
10	16	100.0	428	4	US-09-548-376D-51	Sequence 51, Appl
11	16	100.0	428	4	US-09-794-927A-51	Sequence 51, Appl
12	16	100.0	428	4	US-09-548-373D-51	Sequence 51, Appl
13	16	100.0	428	4	US-09-795-847B-51	Sequence 51, Appl
14	16	100.0	428	4	US-09-869-414-51	Sequence 51, Appl
15	16	100.0	428	4	US-09-548-366F-51	Sequence 51, Appl
16	16	100.0	428	4	US-09-548-368D-51	Sequence 51, Appl
17	16	100.0	428	4	US-09-794-925A-51	Sequence 51, Appl
18	16	100.0	431	4	US-09-724-566A-74	Sequence 74, Appl
19	16	100.0	431	4	US-09-471-669A-74	Sequence 74, Appl
20	16	100.0	433	4	US-09-548-372D-26	Sequence 26, Appl
21	16	100.0	433	4	US-09-548-367D-26	Sequence 26, Appl
22	16	100.0	433	4	US-09-551-853D-26	Sequence 26, Appl
23	16	100.0	433	4	US-09-416-901B-26	Sequence 26, Appl
24	16	100.0	433	4	US-09-548-376D-26	Sequence 26, Appl
25	16	100.0	433	4	US-09-794-927A-26	Sequence 26, Appl
26	16	100.0	433	4	US-09-548-373D-26	Sequence 26, Appl
27	16	100.0	433	4	US-09-795-847B-26	Sequence 26, Appl
28	16	100.0	433	4	US-09-869-414-26	Sequence 26, Appl
29	16	100.0	433	4	US-09-548-366F-26	Sequence 26, Appl
30	16	100.0	433	4	US-09-548-368D-26	Sequence 26, Appl
31	16	100.0	433	4	US-09-794-925A-26	Sequence 26, Appl
32	16	100.0	433	4	US-09-806-194A-26	Sequence 26, Appl
33	16	100.0	434	4	US-09-548-372D-53	Sequence 53, Appl
34	16	100.0	434	4	US-09-548-367D-53	Sequence 53, Appl
35	16	100.0	434	4	US-09-551-853D-53	Sequence 53, Appl
36	16	100.0	434	4	US-09-416-901B-53	Sequence 53, Appl
37	16	100.0	434	4	US-09-548-376D-53	Sequence 53, Appl
38	16	100.0	434	4	US-09-794-927A-53	Sequence 53, Appl
39	16	100.0	434	4	US-09-548-373D-53	Sequence 53, Appl
40	16	100.0	434	4	US-09-795-847B-53	Sequence 53, Appl
41	16	100.0	434	4	US-09-869-414-53	Sequence 53, Appl
42	16	100.0	434	4	US-09-548-366F-53	Sequence 53, Appl
43	16	100.0	434	4	US-09-548-368D-53	Sequence 53, Appl
44	16	100.0	434	4	US-09-794-925A-53	Sequence 53, Appl
45	16	100.0	446	4	US-09-548-372D-22	Sequence 22, Appl

ALIGNMENTS

RESULT 1
US-09-724-566A-47
; Sequence 47, Application US/09724566A
; Patent No. 6627739
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Guriqbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, No. 6627739mand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 228-US-NEWC2
; CURRENT APPLICATION NUMBER: US/09/724,566A
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 47
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-566A-47

Query Match 100.0%; Score 16; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 8e-10;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 TQHGIRLPLRSGLGGA 16
              ||||||||||||||||
Db          1 TQHGIRLPLRSGLGGA 16
```

RESULT 2
US-09-724-566A-57
; Sequence 57, Application US/09724566A
; Patent No. 6627739
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.

```
 ;  APPLICANT:  Basi, Guriqbal
 ;  APPLICANT:  Doane, Minh Tam
 ;  APPLICANT:  Frigon, No. 6627739mand
 ;  APPLICANT:  John, Varghese
 ;  APPLICANT:  Power, Michael
 ;  APPLICANT:  Sinha, Sukanto
 ;  APPLICANT:  Tatsuno, Gwen
 ;  APPLICANT:  Tung, Jay
 ;  APPLICANT:  Wang, Shuwen
 ;  APPLICANT:  McConlogue, Lisa
 ;  TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
 ;  TITLE OF INVENTION:  Methods
 ;  FILE REFERENCE: 228-US-NEWC2
 ;  CURRENT APPLICATION NUMBER: US/09/724,566A
 ;  CURRENT FILING DATE:  2000-11-28
 ;  PRIOR APPLICATION NUMBER: US 09/501,708
 ;  PRIOR FILING DATE: 2000-02-10
 ;  PRIOR APPLICATION NUMBER: 60/119,571
 ;  PRIOR FILING DATE: 1999-02-10
 ;  PRIOR APPLICATION NUMBER: 60/139,172
 ;  PRIOR FILING DATE: 1999-06-15
 ;  NUMBER OF SEQ ID NOS: 104
 ;  SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 57
 ;   LENGTH: 419
 ;   TYPE: PRT
 ;   ORGANISM: Homo sapiens
US-09-724-566A-57

  Query Match             100.0%;  Score 16;  DB 4;  Length 419;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-08;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TQHGIRLPLRSGLGGA 16
              ||||||||||||||||
Db         22 TQHGIRLPLRSGLGGA 37


RESULT 3
US-09-471-669A-57
; Sequence 57, Application US/09471669A
; Patent No. 6830918
; GENERAL INFORMATION:
;  APPLICANT: Anderson, John P.
;  APPLICANT:  Basi, Guriqbal
;  APPLICANT:  Doane, Minh Tam
;  APPLICANT:  Frigon, No. 6830918mand
;  APPLICANT:  John, Varghese
;  APPLICANT:  Power, Michael
;  APPLICANT:  Sinha, Sukanto
;  APPLICANT:  Tatsuno, Gwen
;  APPLICANT:  Tung, Jay
;  APPLICANT:  Wang, Shuwen
;  APPLICANT:  McConlogue, Lisa
;  APPLICANT:  Elan Pharmaceuticals, Inc.
;  TITLE OF INVENTION: BETA-SECRETASE ENZYME COMPOSITIONS AND METHODS
;  FILE REFERENCE: 015270-006430US
;  CURRENT APPLICATION NUMBER: US/09/471,669A
;  CURRENT FILING DATE:  1999-12-24
;  PRIOR APPLICATION NUMBER: US 60/114,408
;  PRIOR FILING DATE: 1998-12-31
;  PRIOR APPLICATION NUMBER: US 60/119,571
;  PRIOR FILING DATE: 1999-02-10
;  PRIOR APPLICATION NUMBER: US 60/139,172
;  PRIOR FILING DATE: 1999-06-15
;  NUMBER OF SEQ ID NOS: 108
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 57
;   LENGTH: 419
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-471-669A-57

  Query Match             100.0%;  Score 16;  DB 4;  Length 419;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-08;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TQHGIRLPLRSGLGGA 16
              ||||||||||||||||
Db         22 TQHGIRLPLRSGLGGA 37


RESULT 4
US-09-724-566A-60
; Sequence 60, Application US/09724566A
; Patent No. 6627739
; GENERAL INFORMATION:
;  APPLICANT: Anderson, John P.
;  APPLICANT:  Basi, Guriqbal
;  APPLICANT:  Doane, Minh Tam
;  APPLICANT:  Frigon, No. 6627739mand
;  APPLICANT:  John, Varghese
;  APPLICANT:  Power, Michael
;  APPLICANT:  Sinha, Sukanto
;  APPLICANT:  Tatsuno, Gwen
;  APPLICANT:  Tung, Jay
;  APPLICANT:  Wang, Shuwen
;  APPLICANT:  McConlogue, Lisa
;  TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
;  TITLE OF INVENTION:  Methods
;  FILE REFERENCE: 228-US-NEWC2
;  CURRENT APPLICATION NUMBER: US/09/724,566A
;  CURRENT FILING DATE:  2000-11-28
;  PRIOR APPLICATION NUMBER: US 09/501,708
;  PRIOR FILING DATE: 2000-02-10
;  PRIOR APPLICATION NUMBER: 60/119,571
;  PRIOR FILING DATE: 1999-02-10
;  PRIOR APPLICATION NUMBER: 60/139,172
;  PRIOR FILING DATE: 1999-06-15
;  NUMBER OF SEQ ID NOS: 104
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 60
;   LENGTH: 420
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-724-566A-60

  Query Match             100.0%;  Score 16;  DB 4;  Length 420;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-08;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TQHGIRLPLRSGLGGA 16
              ||||||||||||||||
Db         22 TQHGIRLPLRSGLGGA 37


RESULT 5
US-09-471-669A-60
; Sequence 60, Application US/09471669A
; Patent No. 6830918
; GENERAL INFORMATION:
;  APPLICANT: Anderson, John P.
;  APPLICANT:  Basi, Guriqbal
;  APPLICANT:  Doane, Minh Tam
;  APPLICANT:  Frigon, No. 6830918mand
;  APPLICANT:  John, Varghese
;  APPLICANT:  Power, Michael
;  APPLICANT:  Sinha, Sukanto
;  APPLICANT:  Tatsuno, Gwen
;  APPLICANT:  Tung, Jay
;  APPLICANT:  Wang, Shuwen
;  APPLICANT:  McConlogue, Lisa
;  APPLICANT:  Elan Pharmaceuticals, Inc.
;  TITLE OF INVENTION: BETA-SECRETASE ENZYME COMPOSITIONS AND METHODS
;  FILE REFERENCE: 015270-006430US
;  CURRENT APPLICATION NUMBER: US/09/471,669A
```

```
;  CURRENT FILING DATE:  1999-12-24
;  PRIOR APPLICATION NUMBER: US 60/114,408
;  PRIOR FILING DATE: 1998-12-31
;  PRIOR APPLICATION NUMBER: US 60/119,571
;  PRIOR FILING DATE: 1999-02-10
;  PRIOR APPLICATION NUMBER: US 60/139,172
;  PRIOR FILING DATE: 1999-06-15
;  NUMBER OF SEQ ID NOS: 108
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 60
;   LENGTH: 420
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-471-669A-60

  Query Match           100.0%;  Score 16;  DB 4;  Length 420;
  Best Local Similarity  100.0%;  Pred. No. 1.1e-08;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TQHGIRLPLRSGLGGA 16
              ||||||||||||||||
Db         22 TQHGIRLPLRSGLGGA 37


RESULT 6
US-09-548-372D-51
; Sequence 51, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
;  APPLICANT: GURNEY ET AL.
;  TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 29915/6280I
;  CURRENT APPLICATION NUMBER: US/09/548,372D
;  CURRENT FILING DATE:  2000-04-12
;  PRIOR APPLICATION NUMBER: US 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 51
;   LENGTH: 428
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Hu-Asp2(b) delta TM
US-09-548-372D-51

  Query Match           100.0%;  Score 16;  DB 4;  Length 428;
  Best Local Similarity  100.0%;  Pred. No. 1.1e-08;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TQHGIRLPLRSGLGGA 16
              ||||||||||||||||
Db         22 TQHGIRLPLRSGLGGA 37


RESULT 7
US-09-548-367D-51
; Sequence 51, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
;  APPLICANT: GURNEY ET AL.
;  TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 29915/6280H
;  CURRENT APPLICATION NUMBER: US/09/548,367D
;  CURRENT FILING DATE:  2000-04-12
;  PRIOR APPLICATION NUMBER: US 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 51
;   LENGTH: 428
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Hu-Asp2(b) delta TM
US-09-548-367D-51

  Query Match           100.0%;  Score 16;  DB 4;  Length 428;
  Best Local Similarity  100.0%;  Pred. No. 1.1e-08;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TQHGIRLPLRSGLGGA 16
              ||||||||||||||||
Db         22 TQHGIRLPLRSGLGGA 37


RESULT 8
US-09-551-853D-51
; Sequence 51, Application US/09551853D
; Patent No. 6500667
; GENERAL INFORMATION:
;  APPLICANT: GURNEY ET AL.
;  TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 29915/6280L
;  CURRENT APPLICATION NUMBER: US/09/551,853D
;  CURRENT FILING DATE:  2000-04-18
;  PRIOR APPLICATION NUMBER: US 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 51
;   LENGTH: 428
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Hu-Asp2(b) delta TM
US-09-551-853D-51

  Query Match           100.0%;  Score 16;  DB 4;  Length 428;
  Best Local Similarity  100.0%;  Pred. No. 1.1e-08;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TQHGIRLPLRSGLGGA 16
              ||||||||||||||||
Db         22 TQHGIRLPLRSGLGGA 37


RESULT 9
US-09-416-901B-51
; Sequence 51, Application US/09416901B
; Patent No. 6699671
; GENERAL INFORMATION:
;  APPLICANT: GURNEY ET AL.
;  TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
;  TITLE OF INVENTION:  THEREOF
```

```
 ;  FILE REFERENCE: 29915/6280A
 ;  CURRENT APPLICATION NUMBER: US/09/416,901B
 ;  CURRENT FILING DATE:  1999-10-13
 ;  PRIOR APPLICATION NUMBER: US 60/155,493
 ;  PRIOR FILING DATE: 1999-09-23
 ;  PRIOR APPLICATION NUMBER: US 09/404,133
 ;  PRIOR FILING DATE: 1999-09-23
 ;  PRIOR APPLICATION NUMBER: PCT/US99/20881
 ;  PRIOR FILING DATE: 1999-09-23
 ;  PRIOR APPLICATION NUMBER: US 60/101,594
 ;  PRIOR FILING DATE: 1998-09-24
 ;  NUMBER OF SEQ ID NOS: 72
 ;  SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 51
 ;   LENGTH: 428
 ;   TYPE: PRT
 ;   ORGANISM: Artificial sequence
 ;   FEATURE:
 ;   OTHER INFORMATION: Hu-Asp2(b) delta TM
US-09-416-901B-51

  Query Match           100.0%;  Score 16;  DB 4;  Length 428;
  Best Local Similarity  100.0%;  Pred. No. 1.1e-08;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TQHGIRLPLRSGLGGA 16
              ||||||||||||||||
Db         22 TQHGIRLPLRSGLGGA 37


RESULT 10
US-09-548-376D-51
; Sequence 51, Application US/09548376D
; Patent No. 6706485
; GENERAL INFORMATION:
;  APPLICANT: GURNEY ET AL.
;  TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR
;  TITLE OF INVENTION:  AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 29915/6280F
;  CURRENT APPLICATION NUMBER: US/09/548,376D
;  CURRENT FILING DATE:  2000-04-12
;  PRIOR APPLICATION NUMBER: US 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 51
;   LENGTH: 428
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Hu-Asp2(b) delta TM
US-09-548-376D-51

  Query Match           100.0%;  Score 16;  DB 4;  Length 428;
  Best Local Similarity  100.0%;  Pred. No. 1.1e-08;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TQHGIRLPLRSGLGGA 16
              ||||||||||||||||
Db         22 TQHGIRLPLRSGLGGA 37


RESULT 11
US-09-794-927A-51
; Sequence 51, Application US/09794927A
; Patent No. 6727074
; GENERAL INFORMATION:
;  APPLICANT: Gurney et al.
;  TITLE OF INVENTION: Alzheimer's Disease Secretase, APP Substrates Therefor and Uses
;  TITLE OF INVENTION:  Therefor
;  FILE REFERENCE: 29915/6280FG
;  CURRENT APPLICATION NUMBER: US/09/794,927A
;  CURRENT FILING DATE:  2001-02-27
;  PRIOR APPLICATION NUMBER: 09/416,901
;  PRIOR FILING DATE: 1999-10-13
;  PRIOR APPLICATION NUMBER: 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 74
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 51
;   LENGTH: 428
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Hu-Asp2(b) delta TM
US-09-794-927A-51

  Query Match           100.0%;  Score 16;  DB 4;  Length 428;
  Best Local Similarity  100.0%;  Pred. No. 1.1e-08;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TQHGIRLPLRSGLGGA 16
              ||||||||||||||||
Db         22 TQHGIRLPLRSGLGGA 37


RESULT 12
US-09-548-373D-51
; Sequence 51, Application US/09548373D
; Patent No. 6737510
; GENERAL INFORMATION:
;  APPLICANT: GURNEY ET AL.
;  TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 29915/6280B
;  CURRENT APPLICATION NUMBER: US/09/548,373D
;  CURRENT FILING DATE:  2000-04-12
;  PRIOR APPLICATION NUMBER: US 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 51
;   LENGTH: 428
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Hu-Asp2(b) delta TM
US-09-548-373D-51

  Query Match           100.0%;  Score 16;  DB 4;  Length 428;
  Best Local Similarity  100.0%;  Pred. No. 1.1e-08;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TQHGIRLPLRSGLGGA 16
              ||||||||||||||||
Db         22 TQHGIRLPLRSGLGGA 37
```

RESULT 13
US-09-795-847B-51
; Sequence 51, Application US/09795847B
; Patent No. 6753163
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280DE
; CURRENT APPLICATION NUMBER: US/09/795,847B
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 51
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Hu-Asp2(b) delta TM
US-09-795-847B-51

Query Match 100.0%; Score 16; DB 4; Length 428;
Best Local Similarity 100.0%; Pred. No. 1.1e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TQHGIRLPLRSGLGGA 16
||||||||||||||||
Db 22 TQHGIRLPLRSGLGGA 37

RESULT 14
US-09-869-414-51
; Sequence 51, Application US/09869414
; Patent No. 6790610
; GENERAL INFORMATION:
; APPLICANT: Beinkowski et al.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280M
; CURRENT APPLICATION NUMBER: US/09/869,414
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 51
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Hu-Asp2(b)
; OTHER INFORMATION: delta TM
US-09-869-414-51

Query Match 100.0%; Score 16; DB 4; Length 428;
Best Local Similarity 100.0%; Pred. No. 1.1e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TQHGIRLPLRSGLGGA 16
||||||||||||||||
Db 22 TQHGIRLPLRSGLGGA 37

RESULT 15
US-09-548-366F-51
; Sequence 51, Application US/09548366F
; Patent No. 6797487
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280J
; CURRENT APPLICATION NUMBER: US/09/548,366F
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 51
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Hu-Asp2(b) delta TM
US-09-548-366F-51

Query Match 100.0%; Score 16; DB 4; Length 428;
Best Local Similarity 100.0%; Pred. No. 1.1e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TQHGIRLPLRSGLGGA 16
||||||||||||||||
Db 22 TQHGIRLPLRSGLGGA 37

Search completed: July 26, 2005, 16:38:50
Job time : 44 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: July 26, 2005, 16:24:19 ; Search time 166 Seconds
(without alignments)
37.278 Million cell updates/sec

Title: US-10-726-967A-3
Perfect score: 16
Sequence: 1 TQHGIRLPLRSGLGGA 16

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2105692 seqs, 386760381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	16	100.0	16	8	ADP83877	Adp83877 Human BAC
2	16	100.0	425	7	ADC81580	Adc81580 Beta-secr
3	16	100.0	428	4	AAU07219	Aau07219 Human asp
4	16	100.0	428	4	AAE10646	Aae10646 Human-Asp
5	16	100.0	428	4	AAE06891	Aae06891 Human-Asp
6	16	100.0	428	4	AAE02598	Aae02598 Human asp
7	16	100.0	428	4	AAU06620	Aau06620 Human-pro
8	16	100.0	428	5	ABB78607	Abb78607 Human Asp
9	16	100.0	428	8	ADJ94363	Adj94363 Human-pro
10	16	100.0	428	8	ADO50459	Ado50459 Human Asp
11	16	100.0	428	8	ADR75372	Adr75372 Human Asp
12	16	100.0	432	7	ADC81561	Adc81561 Mature BA
13	16	100.0	433	3	AAY88433	Aay88433 Human-pro
14	16	100.0	433	4	AAU07213	Aau07213 T7-human
15	16	100.0	433	4	AAE10640	Aae10640 Human-pro
16	16	100.0	433	4	AAE06870	Aae06870 Human-pro
17	16	100.0	433	4	AAE02592	Aae02592 Human-pro
18	16	100.0	433	4	AAU06614	Aau06614 Human-pro
19	16	100.0	433	5	ABB78601	Abb78601 Human-pro
20	16	100.0	433	8	ADJ94338	Adj94338 Human-pro
21	16	100.0	433	8	ADO50434	Ado50434 Human-pro
22	16	100.0	433	8	ADP83954	Adp83954 Human BAC
23	16	100.0	433	8	ADP83951	Adp83951 Human BAC
24	16	100.0	433	8	ADP83957	Adp83957 Human BAC
25	16	100.0	433	8	ADR75347	Adr75347 Human-pro
26	16	100.0	434	4	AAU07220	Aau07220 Human asp
27	16	100.0	434	4	AAE10647	Aae10647 Human-Asp
28	16	100.0	434	4	AAE06892	Aae06892 Human-Asp
29	16	100.0	434	4	AAE02599	Aae02599 Human asp
30	16	100.0	434	4	AAU06621	Aau06621 Human-pro
31	16	100.0	434	5	ABB78608	Abb78608 Human Asp
32	16	100.0	434	8	ADJ94365	Adj94365 Human-pro
33	16	100.0	434	8	ADO50461	Ado50461 Human Asp
34	16	100.0	434	8	ADR75374	Adr75374 Human Asp
35	16	100.0	435	8	ADI64641	Adi64641 Mature hu
36	16	100.0	439	8	ADP83949	Adp83949 Human BAC
37	16	100.0	446	3	AAY88431	Aay88431 T7-caspas
38	16	100.0	446	4	AAU07211	Aau07211 T7-human
39	16	100.0	446	4	AAE10638	Aae10638 T7-Human-
40	16	100.0	446	4	AAE06868	Aae06868 T7-Human-
41	16	100.0	446	4	AAE02590	Aae02590 T7-Human-
42	16	100.0	446	4	AAU06612	Aau06612 Human T7-
43	16	100.0	446	5	ABB78599	Abb78599 T7-human-
44	16	100.0	446	8	ADJ94334	Adj94334 Human T7-
45	16	100.0	446	8	ADO50430	Ado50430 T7-Human-

ALIGNMENTS

RESULT 1
ADP83877
ID ADP83877 standard; peptide; 16 AA.
XX
AC ADP83877;
XX
DT 23-SEP-2004 (first entry)
XX
DE Human BACE1 22-37 prodomain amino acid sequence SEQ ID NO:2.
XX
KW human; beta-site amyloid precursor protein cleaving enzyme 1;
KW beta-site APP cleaving enzyme 1; BACE1; BACE1 isoform A; chromosome 11;
KW prodomain; engineered cleavage site; protease domain; neuroprotective;
KW nootropic; gene therapy; Alzheimer's disease; Down's syndrome.
XX
OS Homo sapiens.
XX
PN WO2004056962-A2.
XX
PD 08-JUL-2004.
XX
PF 02-DEC-2003; 2003WO-US038314.
XX
PR 04-DEC-2002; 2002US-0430984P.
XX
PA (SUNE-) SUNESIS PHARM INC.
XX
PI Ballinger M;
XX
DR WPI; 2004-507703/48.
XX
PT New polypeptides for producing homogenously processed preparations of
PT beta site amyloid precursor protein-cleaving enzyme comprises a
PT prodomain, an engineered cleavage site and a protease domain.
XX
PS Claim 1; SEQ ID NO 3; 40pp; English.
XX
CC The present invention describes a polypeptide (I) comprising in order
CC from the N-terminus to the C-terminus: (a) a prodomain comprising at
CC least 6 contiguous amino acids of the 16 amino acid sequence of SEQ ID
CC NO:3 (ADP83877, comprising residues 22-37 of SEQ ID NO:1 (ADP83876) which
CC is the longest isoform of human beta-site amyloid precursor protein (APP)
CC cleaving enzyme 1 (BACE1), isoform A); (b) an engineered cleavage site;
CC and (c) a protease domain. (I) is capable of being cleaved at the
CC engineered cleavage site, and so releases a free protease domain that has
CC BACE1 activity. Also described: (1) a nucleic acid sequence encoding (I);
CC (2) a vector for expression of (I); and (3) a host cell expressing (I).
CC (I) has neuroprotective and nootropic activities, and can be used in gene

CC therapy. (I) can be used for producing preparations of homogenously
CC processed BACE that may be used for e.g. studying or treating diseases
CC such as Alzheimer's disease or Down's syndrome. The human BACE1 gene is
CC located on chromosome 11, more specifically to 11q23.2-23.3. The present
CC sequence represents the human BACE1 isoform A 22-37 prodomain amino acid
CC sequence, which is used in the exemplification of the present invention.
XX
SQ Sequence 16 AA;

Query Match 100.0%; Score 16; DB 8; Length 16;
Best Local Similarity 100.0%; Pred. No. 7e-09;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TQHGIRLPLRSGLGGA 16
||||||||||||||||
Db 1 TQHGIRLPLRSGLGGA 16

RESULT 2
ADC81580
ID ADC81580 standard; protein; 425 AA.
XX
AC ADC81580;
XX
DT 01-JAN-2004 (first entry)
XX
DE Beta-secretase zymogen (pbsz) amino acid sequence SEQ ID NO:3.
XX
KW human; BACE; modification; Pro33Lys; pro-enzyme.
XX
OS Unidentified.
XX
PN WO2003072733-A2.
XX
PD 04-SEP-2003.
XX
PF 21-FEB-2003; 2003WO-US005508.
XX
PR 21-FEB-2002; 2002US-0358651P.
XX
PA (PHAA) PHARMACIA & UPJOHN CO.
XX
PI Chou K, Howe JW;
XX
DR WPI; 2003-712719/67.
XX
PT BACE polypeptides having Pro33Lys modification, useful in determining
PT possible mutations, which will inhibit enzyme activity, and in
PT determining potential active site for target molecules.
XX
PS Disclosure; Fig 3; 38pp; English.
XX
CC The present invention describes an isolated polypeptide (I) comprising or
CC consisting of a fully defined sequence of 432 amino acids (see ADC81561),
CC and comprising human BACE having the modification Pro33Lys. Also
CC described: (1) a composition comprising an active human BACE enzyme
CC comprising the pro-enzyme sequence of BACE having the modification
CC Pro33Lys; (2) an isolated polynucleotide comprising a sequence encoding
CC (I); (3) an isolated polynucleotide consisting or comprising of
CC nucleotides 70-1365 of a 1355-bp sequence (see ADC81562); (4) an
CC expression vector comprising the polynucleotide of (2), or a
CC polynucleotide sequence encoding a Pro33Lys-BACE polypeptide, where the
CC expression vector can produce the Pro33Lys-BACE polypeptide when present
CC in a compatible host cell, when cultured under conditions that allow
CC production; (5) a recombinant host cell comprising the expression vector;
CC and (6) producing a (active) Pro33Lys-BACE polypeptide. The BACE
CC polypeptide having Pro33Lys modification may be used in determining
CC possible mutations, which will inhibit enzyme activity, and in
CC determining potential active site for target molecules. The vector
CC comprising the BACE polynucleotide is useful for producing recombinant
CC BACE polypeptides having Pro33Lys modification. The present sequence
CC represents a beta-secretase zymogen amino acid sequence, which is used in
CC the exemplification of the present invention.
XX
SQ Sequence 425 AA;

Query Match 100.0%; Score 16; DB 7; Length 425;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TQHGIRLPLRSGLGGA 16
||||||||||||||||
Db 1 TQHGIRLPLRSGLGGA 16

RESULT 3
AAU07219
ID AAU07219 standard; protein; 428 AA.
XX
AC AAU07219;
XX
DT 24-OCT-2001 (first entry)
XX
DE Human aspartyl protease 2b deltaTM (HuAsp-2bdeltaTM).
XX
KW Human; aspartyl protease 1; Asp-1; nootropic; neuroprotective;
KW aspartyl protease 2; Asp2; amyloid protein precursor; APP;
KW beta-secretase; Alzheimer's disease; HuAsp-2bdeltaTM.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 1
FT /note= "Encoded by NNN"
FT Misc-difference 2
FT /note= "Encoded by NNC"
FT Misc-difference 61
FT /note= "Encoded by NNN"
FT Misc-difference 62
FT /note= "Encoded by NNC"
FT Misc-difference 121
FT /note= "Encoded by NNN"
FT Misc-difference 122
FT /note= "Encoded by NNG"
FT Misc-difference 181
FT /note= "Encoded by NNN"
FT Misc-difference 182
FT /note= "Encoded by NNG"
FT Misc-difference 241
FT /note= "Encoded by NNN"
FT Misc-difference 242
FT /note= "Encoded by NNC"
FT Misc-difference 301
FT /note= "Encoded by NNN"
FT Misc-difference 302
FT /note= "Encoded by NNT"
XX
PN WO200149097-A2.
XX
PD 12-JUL-2001.
XX
PF 09-MAY-2001; 2001WO-IB000797.
XX
PR 09-MAY-2001; 2001WO-IB000797.
XX
PA (BIEN/) BIENKOWSKI M J.
PA (GURN/) GURNEY M E.
PA (HEIN/) HEINRIKSON R L.
PA (PARO/) PARODI L A.
PA (YANR/) YAN R.
XX
PI Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;
XX
DR WPI; 2001-502548/55.
DR N-PSDB; AAS11732.
XX

PT Novel purified polypeptide comprising fragment of mammalian aspartyl
PT protease 2, lacking Asp2 transmembrane domain and retaining beta
PT secretase activity of Asp2 useful for identifying inhibitors of Asp2
PT activity.
XX
PS Claim 149; Page 167-168; 185pp; English.
XX
CC The invention relates to a novel purified polypeptide comprising a
CC fragment of mammalian aspartyl protease 2 (Asp2) protein which lacks the
CC Asp2 transmembrane domain and the Asp2 protein, and where the polypeptide
CC and the fragment retain the beta-secretase activity of the mammalian Asp2
CC protein. Also included is an isoform of amyloid protein precursor (APP)
CC comprising the amino acid sequence of a APP or its fragment containing an
CC APP cleavage site recognisable by a mammalian beta-secretase, and further
CC comprising two lysine residues at the carboxyl terminus of the amino acid
CC sequence of the mammalian APP or APP fragment. The polypeptides are used
CC for assaying for modulators of beta-secretase activity; identifying
CC agents that inhibit the APP processing activity of human Asp2 aspartyl
CC protease (Hu-Asp2); identifying agents that modulate the activity of Asp2
CC ; and for reducing cellular production of amyloid beta (Abeta) from APP.
CC Agents identified by the above methods are useful for treating
CC Alzheimer's disease; and for identifying modulators of amyloid-beta
CC (Abeta) peptide production, for use in designing therapeutics for the
CC treatment or prevention of Alzheimer's disease. Probes and primers
CC derived from Asp nucleic acid sequences are useful for detecting Hu-Asp
CC nucleic acids in in vitro assays and in Northern and Southern blots. The
CC present sequence represents the amino acid sequence of human Asp-2b delta
CC TM construct which lacks the transmembrane domain. This construct was
CC used for bacterial expression and purification of human Asp2b
XX
SQ Sequence 428 AA;

Query Match 100.0%; Score 16; DB 4; Length 428;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TQHGIRLPLRSGLGGA 16
||||||||||||||||
Db 22 TQHGIRLPLRSGLGGA 37

RESULT 4
AAE10646
ID AAE10646 standard; protein; 428 AA.
XX
AC AAE10646;
XX
DT 10-DEC-2001 (first entry)
XX
DE Human-Asp 2(b) protein lacking transmembrane domain.
XX
KW Human; aspartyl protease 2b; Asp2b; amyloid precursor protein; APP;
KW Alzheimer's disease; AD; dementia; neurofibrillary tangle; gliosis;
KW amyloid plaque; neuronal loss; proteolytic; nootropic; neuroprotective.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN GB2357767-A.
XX
PD 04-JUL-2001.
XX
PF 22-SEP-2000; 2000GB-00023315.
XX
PR 23-SEP-1999; 99US-00404133.
PR 23-SEP-1999; 99US-0155493P.
PR 23-SEP-1999; 99WO-US020881.
PR 13-OCT-1999; 99US-00416901.
PR 06-DEC-1999; 99US-0169232P.
XX
PA (PHAA) PHARMACIA & UPJOHN CO.
XX
PI Bienkowkski MJ, Gurney M;
XX
DR WPI; 2001-444208/48.
DR N-PSDB; AAD17895.
XX
PT Polypeptide comprising fragments of human aspartyl protease with amyloid
PT precursor protein processing activity and alpha-secretase activity, for
PT identifying modulators useful in treating Alzheimer's disease.
XX
PS Example 10; Page 138-139; 187pp; English.
XX
CC The patent discloses human aspartyl protease 1 (hu-Asp1) or modified Asp1
CC proteins which lack transmembrane domain or amino terminal domain or
CC cytoplasmic domain and retains alpha-secretase activity and amyloid
CC protein precursor (APP) processing activity. The proteins of the
CC invention are useful for assaying hu-Asp1 alpha-secretase activity, which
CC in turn is useful for identifying modulators of hu-Asp1 alpha-secretase
CC activity, where modulators that increase hu-Asp1 alpha-secretase activity
CC are useful for treating Alzheimer's disease (AD) which causes progressive
CC dementia with consequent formation of amyloid plaques, neurofibrillary
CC tangles, gliosis and neuronal loss. Hu-Asp1 protease substrate is useful
CC for assaying hu-Asp1 proteolytic activity, by contacting hu-Asp1 protein
CC with the substrate under acidic conditions and determining the level of
CC hu-Asp1 proteolytic activity. The present sequence is human Asp 2(b)
CC protein lacking a transmembrane (TM) domain. This sequence is generated
CC by the deletion of the C-terminal TM domain and intracellular domains of
CC human Asp 2(b) protein
XX
SQ Sequence 428 AA;

Query Match 100.0%; Score 16; DB 4; Length 428;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TQHGIRLPLRSGLGGA 16
||||||||||||||||
Db 22 TQHGIRLPLRSGLGGA 37

RESULT 5
AAE06891
ID AAE06891 standard; protein; 428 AA.
XX
AC AAE06891;
XX
DT 23-OCT-2001 (first entry)
XX
DE Human-Asp2(b) deltaTM protein.
XX
KW Human; aspartyl protease 2b; Asp 2b; beta-amyloid precursor protein; APP;
KW beta-secretase; Alzheimer's disease; dementia; amyloid plaque; gliosis;
KW neurofibrillary tangle; neuronal loss; amyloid-beta peptide; nootropic;
KW neuroprotective; antisense therapy; Asp2(b) deltaTM protein;
KW gene therapy.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200150829-A2.
XX
PD 19-JUL-2001.
XX
PF 09-MAY-2001; 2001WO-IB000799.
XX
PR 09-MAY-2001; 2001WO-IB000799.
XX
PA (BIEN/) BIENKOWSKI M J.
PA (GURN/) GURNEY M E.
PA (HEIN/) HEINRIKSON R L.
PA (PARO/) PARODI L A.
PA (YANR/) YAN R.
XX
PI Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;
XX

DR WPI; 2001-483072/52.
DR N-PSDB; AAD13276.
XX
PT Novel purified polypeptide comprising fragment of mammalian aspartyl
PT protease 2, lacking Asp2 transmembrane domain and retaining beta
PT secretase activity of Asp2 useful for identifying inhibitors of Asp2
PT activity.
XX
PS Claim 149; Page 167-168; 185pp; English.
XX
CC The invention relates to human aspartyl proteases (Hu-Asp), beta-amyloid
CC precursor protein (APP) isoforms and their corresponding DNA molecules.
CC Human aspartyl proteases can act as beta-secretase proteases useful for
CC treating Alzheimer's disease. APP isoforms are useful for identifying
CC modulators of amyloid-beta peptide production, for use in designing
CC therapeutics for the treatment and prevention of Alzheimer's disease,
CC dementia, formation of amyloid plaques, neurofibrillary tangles, gliosis
CC and neuronal loss. APP isoforms are also used in methods for identifying
CC inhibitors and modulators of human Asp2 activity. The invention relates
CC to a method for identifying agents that modulate the activity of human
CC aspartyl protease Asp2. Amyloid-beta peptides obtained from APP are used
CC as a means to screen in cellular assays for the inhibitors of beta- and
CC gamma- secretase. Hu-Asp DNA fragments are useful as probes or primers in
CC polymerase chain reactions (PCR). The probes are useful for detecting Hu-
CC Asp nucleic acids in in vitro assays and in Northern and Southern blots.
CC The present sequence is Human aspartyl protease 2b (Hu-Asp2b) deltaTM
CC protein which is obtained by the deletion of C-terminal transmembrane and
CC intracellular domains of Hu-Asp2b. Human Asp2b has beta-secretase
CC activity
XX
SQ Sequence 428 AA;

Query Match 100.0%; Score 16; DB 4; Length 428;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TQHGIRLPLRSGLGGA 16
||||||||||||||||
Db 22 TQHGIRLPLRSGLGGA 37

RESULT 6
AAE02598
ID AAE02598 standard; protein; 428 AA.
XX
AC AAE02598;
XX
DT 10-AUG-2001 (first entry)
XX
DE Human aspartyl protease 2 (b) delta TM protein.
XX
KW Human; alpha-secretase; amyloid precursor protein; APP; therapy;
KW Alzheimer's disease; antialzheimer's; aspartyl protease 2; Asp 2;
KW beta-secretase; chromosome 11q23.3-24.1; mutant; mutein.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200123533-A2.
XX
PD 05-APR-2001.
XX
PF 22-SEP-2000; 2000WO-US026080.
XX
PR 23-SEP-1999; 99US-0155493P.
PR 23-SEP-1999; 99WO-US020881.
PR 13-OCT-1999; 99US-00416901.
PR 06-DEC-1999; 99US-0169232P.
XX
PA (PHAA) PHARMACIA & UPJOHN CO.
XX
PI Gurney M, Bienkowski MJ;
XX

DR WPI; 2001-290516/30.
DR N-PSDB; AAD06768.
XX
PT Enzymes that cleave the alpha-secretase site of the amyloid precursor
PT protein, useful for the treatment of Alzheimer's disease.
XX
PS Example 10; Page 166-167; 189pp; English.
XX
CC The present invention relates to enzymes for cleaving the alpha-
CC secretase site of the amyloid precursor protein (APP) and methods of
CC identifying those enzymes. The methods may be used to identify enzymes
CC that may be used to cleave the alpha-secretase cleavage site of the APP
CC protein. The enzymes may be used to treat or modulate the progress of
CC Alzheimer's disease. The present sequence is human aspartyl protease 2
CC (Asp 2) (b) delta TM protein. The Asp 2 gene is located on chromosome
CC 11q23.3-24.1. The Asp 2 has beta-secretase protease activity
XX
SQ Sequence 428 AA;

Query Match 100.0%; Score 16; DB 4; Length 428;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TQHGIRLPLRSGLGGA 16
||||||||||||||||
Db 22 TQHGIRLPLRSGLGGA 37

RESULT 7
AAU06620
ID AAU06620 standard; protein; 428 AA.
XX
AC AAU06620;
XX
DT 24-OCT-2001 (first entry)
XX
DE Human-pro-Asp 2(b) delta TM.
XX
KW Human; Aspartyl protease; beta-secretase; nootropic; ASP2;
KW neuroprotective; amyloid protein precursor; APP; Alzheimer's disease;
KW amyloid-beta; Abeta; Human-pro-Asp 2(b) delta TM; mutant; mutein.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200149098-A2.
XX
PD 12-JUL-2001.
XX
PF 09-MAY-2001; 2001WO-IB000798.
XX
PR 09-MAY-2001; 2001WO-IB000798.
XX
PA (BIEN/) BIENKOWSKI M J.
PA (GURN/) GURNEY M E.
PA (HEIN/) HEINRIKSON R L.
PA (PARO/) PARODI L A.
PA (YANR/) YAN R.
XX
PI Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;
XX
DR WPI; 2001-502549/55.
XX
PT Novel purified polypeptide comprising fragment of mammalian aspartyl
PT protease 2, lacking Asp2 transmembrane domain and retaining beta
PT secretase activity of Asp2 useful for identifying inhibitors of Asp2
PT activity.
XX
PS Claim 149; Page 167-168; 185pp; English.
XX
CC The invention relates to a purified polypeptide comprising a fragment of
CC mammalian aspartyl protease (Asp)2 protein which lacks the Asp2
CC transmembrane domain and the Asp2 protein, and where the polypeptide and

CC the fragment retain the beta-secretase activity of the mammalian Asp2
CC protein. The invention also details polynucleotides for the Asp proteins
CC and vectors expressing them, and a polypeptide (isoform of amyloid
CC protein precursor (APP)) comprising the amino acid sequence of an APP or
CC its fragment containing an APP cleavage site recognizable by a mammalian
CC beta-secretase, and further comprising two lysine residues at the
CC carboxyl terminus of the amino acid sequence of the mammalian APP or APP
CC fragment. Also included in the invention are methods of identifying
CC modulators or inhibitors of Asp2. Modulators and inhibitors of Asp2 are
CC useful for treating Alzheimer's disease. APP is useful in methods for
CC identifying inhibitors or modulators of human Asp2 activity and amyloid-
CC beta (Abeta) peptide production. APP is also useful in designing
CC therapeutics for the treatment or prevention of Alzheimer's disease. APP
CC comprising the APP-Sw-beta-secretase peptide sequence (NLDA), which is
CC associated with increased levels of Abeta processing is useful in assays
CC relating the Alzheimer's research. The expression vector is useful for
CC recombinantly expressing APP. Nucleic acids that hybridise to Asp
CC oligonucleotides are useful as probes or primers. The probes are useful
CC for detecting Hu-Asp nucleic acids in in vitro assays and in Northern and
CC Southern blots. The present sequence is Human-pro- Asp 2(b) delta TM
CC protein, which lacks the C-terminal transmembrane domain
XX
SQ Sequence 428 AA;

```
  Query Match             100.0%;  Score 16;  DB 4;  Length 428;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-07;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TQHGIRLPLRSGLGGA 16
              ||||||||||||||||
Db         22 TQHGIRLPLRSGLGGA 37
```

RESULT 8
ABB78607
ID ABB78607 standard; protein; 428 AA.
XX
AC ABB78607;
XX
DT 16-JUL-2002 (first entry)
XX
DE Human Asp-2(b)deltaTM protein sequence SEQ ID NO:51.
XX
KW Human; Asp-1; Asp-2; aspartyl protease; Alzheimer's disease; proteolytic;
KW chromosome 11q23.3-24.1.
XX
OS Homo sapiens.
XX
PN GB2367060-A.
XX
PD 27-MAR-2002.
XX
PF 29-OCT-2001; 2001GB-00025934.
XX
PR 23-SEP-1999; 99US-00404133.
PR 23-SEP-1999; 99US-0155493P.
PR 23-SEP-1999; 99WO-US020881.
PR 13-OCT-1999; 99US-00416901.
PR 06-DEC-1999; 99US-0169232P.
PR 22-SEP-2000; 2000GB-00023315.
XX
PA (PHAA) PHARMACIA & UPJOHN CO.
XX
PI Bienkowkski MJ, Gurney M;
XX
DR WPI; 2002-397167/43.
DR N-PSDB; ABL52487.
XX
PT Human aspartyl protease 1 substrates useful in assays to detect aspartyl
PT protease activity, e.g. for the diagnosis of Alzheimer's disease.
XX
PS Example 10; Page 138-139; 182pp; English.
XX

CC The present invention describes a human aspartyl protease 1 (hu-Asp1)
CC substrate (I) which comprises a peptide of no more than 50 amino acids,
CC and which comprises the 8 amino acid sequence Gly-Leu-Ala-Leu-Ala-Leu-
CC Glu-Pro. Also described are: (1) a method (II) for assaying hu-Asp1
CC proteolytic activity, comprising: (a) contacting a hu-Asp1 protein with
CC (I) under acidic conditions; and (b) determining the level of hu-Asp1
CC proteolytic activity; (2) a purified polynucleotide (III) comprising a
CC nucleotide sequence that hybridises under stringent conditions to the non
CC -coding strand complementary to a defined 1804 nucleotide sequence (see
CC ABL52456) where the nucleotide sequence encodes a polypeptide having Asp1
CC proteolytic activity and lacks nucleotides encoding a transmembrane
CC domain); (3) a purified polynucleotide (III') comprising a sequence that
CC hybridises under stringent conditions to (III) (the nucleotide sequence
CC encodes a polypeptide further lacking a pro-peptide domain corresponding
CC to amino acids 23-62 of hu-Asp1 (see ABB78589)); (4) a vector (IV)
CC comprising (III) or (III'); and (5) a host cell (V) transformed or
CC transfected with (III), (III') and/or (IV). The hu-Asp1 protease
CC substrate (I) may be used as an enzyme substrate in assays to detect
CC aspartyl protease activity, (II) and therefore diagnose diseases
CC associated with aberrant hu-Asp1 expression and activity such as
CC Alzheimer's disease. Hu-Asp1 has been localised to chromosome 21, while
CC hu-Asp2 has been localised to chromosome 11q23.3-24.1. The present
CC sequence represents human Asp-2(b)deltaTM, which is given in an example
CC from the present invention
XX
SQ Sequence 428 AA;

```
  Query Match             100.0%;  Score 16;  DB 5;  Length 428;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-07;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TQHGIRLPLRSGLGGA 16
              ||||||||||||||||
Db         22 TQHGIRLPLRSGLGGA 37
```

RESULT 9
ADJ94363
ID ADJ94363 standard; protein; 428 AA.
XX
AC ADJ94363;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human-pro-Asp-2(b)deltaTM.
XX
KW Human; enzyme; aspartyl protease; Asp-1; Asp-2(a); Asp-2(b);
KW beta secretase; amyloid protein precursor; APP; Alzheimer's disease;
KW nootropic; neuroprotective; amyloid beta; mutant; mutein.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN US6706485-B1.
XX
PD 16-MAR-2004.
XX
PF 12-APR-2000; 2000US-00548376.
XX
PR 24-SEP-1998; 98US-0101594P.
PR 23-SEP-1999; 99US-00404133.
PR 23-SEP-1999; 99US-0155493P.
PR 23-SEP-1999; 99WO-US020881.
PR 13-OCT-1999; 99US-00416901.
XX
PA (PHAA) PHARMACIA & UPJOHN CO.
XX
PI Gurney ME, Bienkowski MJ, Heinrikson RL, Parodi LA, Yan R;
XX
DR WPI; 2004-236722/22.
DR N-PSDB; ADJ94362.
XX
PT Identifying agents that modulate activity of Asp2 aspartyl protease

PT useful for treating or preventing Alzheimer's disease involves comparing
PT APP processing activity of protease in presence and absence of test
PT agent.
XX
PS Example 10; SEQ ID NO 51; 109pp; English.
XX
CC The invention relates to identifying agents that modulate activity of
CC Asp2 (e.g. a beta-secretase, e.g. human Asp-2(b) appearing as ID 6,
CC encoded by ID 5) aspartyl protease, involves contacting Asp2 with amyloid
CC precursor protein (APP) in the presence and absence of a test agent,
CC where Asp2 is a recombinant polypeptide and processes APP into amyloid
CC beta, determining APP processing activity of Asp2 in presence and absence
CC of the test agent, and comparing the activities to identify agents that
CC modulate the activity of Asp2. Also disclosed are the cDNA and proteins
CC for human Asp-1 and Asp-2(a), mouse Asp-2(b), a vector comprising the
CC nucleic acid encoding Hu-Asp2 protease sequence, a host cell comprising
CC the vector and the method of producing Hu-Asp polypeptide, an isolated
CC antibody that specifically binds to Hu-Asp polypeptides, identifying a
CC cell that can be used to screen for inhibitors of beta secretase
CC activity, novel isoforms of amyloid protein precursor (APP), where the
CC last 2 carboxy terminus amino acids of that isoform are both lysine
CC residues (e.g. those designated APP695-KK or carrying the Swedish
CC mutation where KM at 595-596 is mutated to NL, designated e.g. APP695-Sw
CC or APP695-Sw-KK, or a V to F mutation at 642, e.g. APP695-VF, all useful
CC for assaying for beta secretase activity and screening for inhibitors of
CC beta-secretase) and polynucleotides that encode the APP proteins. The
CC method is useful for identifying agents that modulate the activity
CC (amyloid precursor protein processing activity) of Asp2 aspartyl
CC protease. Preferably, the method is useful for identifying agents that
CC inhibit Asp2 aspartyl protease activity. The inhibitors of amyloid
CC precursor protein processing, are useful for treating or preventing
CC Alzheimer's disease. The present sequence represents an aspartyl protease
CC mutant construct (e.g. lacking a transmembrane domain and/or including a
CC caspase cleavage site) used to investigate the cleavage activity of Asp2
CC proteins.
XX
SQ Sequence 428 AA;

Query Match 100.0%; Score 16; DB 8; Length 428;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TQHGIRLPLRSGLGGA 16
||||||||||||||||
Db 22 TQHGIRLPLRSGLGGA 37

RESULT 10
ADO50459
ID ADO50459 standard; protein; 428 AA.
XX
AC ADO50459;
XX
DT 29-JUL-2004 (first entry)
XX
DE Human Asp2(b)deltaTM mutant protein.
XX
KW Aspartyl protease; Asp; beta secretase; amyloid precursor protein; APP;
KW Alzheimer's disease; gene therapy; human; mutant; mutein.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN US6737510-B1.
XX
PD 18-MAY-2004.
XX
PF 12-APR-2000; 2000US-00548373.
XX
PR 24-SEP-1998; 98US-0101594P.
PR 23-SEP-1999; 99US-00404133.
PR 23-SEP-1999; 99US-0155493P.
PR 23-SEP-1999; 99WO-US020881.
PR 13-OCT-1999; 99US-00416901.
XX
PA (PHAA) PHARMACIA & UPJOHN CO.
XX
PI Gurney ME, Bienkowski MJ, Heinrikson RL, Parodi LA, Yan R;
XX
DR WPI; 2004-387112/36.
DR N-PSDB; ADO50458.
XX
PT New Asp2 aspartyl protease protein comprising tripeptides DTG and DSG
PT involved in processing amyloid precursor protein into amyloid beta,
PT useful in preparing a composition for treating or preventing Alzheimer's
PT disease.
XX
PS Example 10; SEQ ID NO 51; 108pp; English.
XX
CC The invention relates to a method for identifying an agent that decreases
CC the protease activity of the aspartyl protease (Asp) polypeptide. It also
CC provides enzyme and enzymatic procedures for cleaving the beta secretase
CC cleavage site of the amyloid precursor protein (APP). The invention is
CC useful in preparing a composition for treating or preventing Alzheimer's
CC disease. It is also useful in gene therapy. The present sequence is human
CC Asp2(b) mutant protein. This sequence is used to illustrate the method of
CC the invention.
XX
SQ Sequence 428 AA;

Query Match 100.0%; Score 16; DB 8; Length 428;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TQHGIRLPLRSGLGGA 16
||||||||||||||||
Db 22 TQHGIRLPLRSGLGGA 37

RESULT 11
ADR75372
ID ADR75372 standard; protein; 428 AA.
XX
AC ADR75372;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human Asp2(b)deltaTM mutant protein.
XX
KW Aspartyl protease; Asp; amyloid precursor protein; APP; amyloid beta;
KW chromosome identification; Alzheimer's disease; human; mutant.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN US2004166507-A1.
XX
PD 26-AUG-2004.
XX
PF 29-AUG-2003; 2003US-00652045.
XX
PR 24-SEP-1998; 98US-0101594P.
PR 23-SEP-1999; 99US-00404133.
PR 23-SEP-1999; 99US-0155493P.
PR 13-OCT-1999; 99US-00416901.
XX
PA (GURN/) GURNEY M E.
PA (BIEN/) BIENKOWAKI M J.
PA (HEIN/) HEINRIKSON R L.
PA (PARO/) PARODI L A.
PA (YANR/) YAN R.
XX
PI Gurney ME, Bienkowaki MJ, Heinrikson RL, Parodi LA, Yan R;
XX
DR WPI; 2004-624916/60.
DR N-PSDB; ADR75371.

```
XX
PT   Novel purified/isolated polynucleotide encoding polypeptide having
PT   aspartyl protease activity involved in processing amyloid precursor
PT   protein into amyloid beta, useful in identifying agent decreasing
PT   activity of aspartyl protease.
XX
PS   Example 10; SEQ ID NO 51; 107pp; English.
XX
CC   The invention relates to nucleic acid sequences encoding aspartyl
CC   protease (Asp) polypeptides having aspartyl protease activity involved in
CC   processing amyloid precursor protein (APP) into amyloid beta. The
CC   invention also relates to a method for identifying an agent that
CC   decreases the protease activity of the Asp. Asp DNA is useful in
CC   chromosome identification as they can hybridise with a specific location
CC   on a human chromosome and in identifying the relationship between genes
CC   and diseases (particular gene responsible for causing diseases). It is
CC   also useful for identifying candidates to modulate the progression of
CC   Alzheimer's disease. Asp is useful in raising antibodies that are useful
CC   in diagnostic assay for detecting Hu-Asp polypeptide expression. The
CC   present sequence is the human Asp2(b)deltaTM mutant protein. This
CC   sequence is used to illustrate the method of the invention.
XX
SQ   Sequence 428 AA;

  Query Match             100.0%;  Score 16;  DB 8;  Length 428;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-07;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TQHGIRLPLRSGLGGA 16
              ||||||||||||||||
Db         22 TQHGIRLPLRSGLGGA 37


RESULT 12
ADC81561
ID   ADC81561 standard; protein; 432 AA.
XX
AC   ADC81561;
XX
DT   01-JAN-2004  (first entry)
XX
DE   Mature BACE P33K amino acid sequence SEQ ID NO:2.
XX
KW   human; BACE; modification; Pro33Lys; pro-enzyme.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO2003072733-A2.
XX
PD   04-SEP-2003.
XX
PF   21-FEB-2003; 2003WO-US005508.
XX
PR   21-FEB-2002; 2002US-0358651P.
XX
PA   (PHAA ) PHARMACIA & UPJOHN CO.
XX
PI   Chou K,  Howe JW;
XX
DR   WPI; 2003-712719/67.
DR   N-PSDB; ADC81562.
XX
PT   BACE polypeptides having Pro33Lys modification, useful in determining
PT   possible mutations, which will inhibit enzyme activity, and in
PT   determining potential active site for target molecules.
XX
PS   Claim 10; SEQ ID NO 2; 38pp; English.
XX
CC   The present invention describes an isolated polypeptide (I) comprising or
CC   consisting of a fully defined sequence of 432 amino acids (see ADC81561),
CC   and comprising human BACE having the modification Pro33Lys. Also
CC   described: (1) a composition comprising an active human BACE enzyme
CC   comprising the pro-enzyme sequence of BACE having the modification
CC   Pro33Lys; (2) an isolated polynucleotide comprising a sequence encoding
CC   (I); (3) an isolated polynucleotide consisting or comprising of
CC   nucleotides 70-1365 of a 1355-bp sequence (see ADC81562); (4) an
CC   expression vector comprising the polynucleotide of (2), or a
CC   polynucleotide sequence encoding a Pro33Lys-BACE polypeptide, where the
CC   expression vector can produce the Pro33Lys-BACE polypeptide when present
CC   in a compatible host cell, when cultured under conditions that allow
CC   production; (5) a recombinant host cell comprising the expression vector;
CC   and (6) producing a (active) Pro33Lys-BACE polypeptide. The BACE
CC   polypeptide having Pro33Lys modification may be used in determining
CC   possible mutations, which will inhibit enzyme activity, and in
CC   determining potential active site for target molecules. The vector
CC   comprising the BACE polynucleotide is useful for producing recombinant
CC   BACE polypeptides having Pro33Lys modification. The present sequence
CC   represents the mature recombinant BACE P33K amino acid sequence used in
CC   the exemplification of the present invention.
XX
SQ   Sequence 432 AA;

  Query Match             100.0%;  Score 16;  DB 7;  Length 432;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-07;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TQHGIRLPLRSGLGGA 16
              ||||||||||||||||
Db          1 TQHGIRLPLRSGLGGA 16


RESULT 13
AAY88433
ID   AAY88433 standard; protein; 433 AA.
XX
AC   AAY88433;
XX
DT   12-SEP-2003  (revised)
DT   06-AUG-2003  (revised)
DT   03-AUG-2000  (first entry)
XX
DE   Human-pro-Asp-2(a)-deltaTM amino acid sequence.
XX
KW   Aspartyl protease; aspartase; amyloid precursor protein; APP; Asp 2;
KW   Alzheimer's disease; beta secretase site; human-pro-Asp-2(a)-deltaTM.
XX
OS   Homo sapiens.
OS   Enterobacteria phage T7.
OS   Chimeric.
XX
PN   WO200017369-A2.
XX
PD   30-MAR-2000.
XX
PF   23-SEP-1999;   99WO-US020881.
XX
PR   24-SEP-1998;   98US-0101594P.
XX
PA   (PHAA ) PHARMACIA & UPJOHN CO.
XX
PI   Gurney ME,  Bienkowski MJ,  Heinrikson RL,  Parodi LA,  Yan R;
XX
DR   WPI; 2000-303209/26.
DR   N-PSDB; AAA15670.
XX
PT   New enzyme designated human aspartase useful in research into Alzheimer's
PT   Disease is capable of cleaving amyloid protein precursor at the beta
PT   secretase site to produce amyloid beta peptide.
XX
PS   Example 9; Fig 8; 183pp; English.
XX
CC   This sequence represents a modified version of the human aspartase 2
CC   (Asp2) amino acid sequence. The sequence is used in the bacterial
CC   expression of human Asp2L. The invention relates to a protease (e.g.
CC   Asp2) capable of cleaving the beta secretase site of amyloid precursor
```

CC protein (APP). The protease contains a sequence encoding the amino acid
CC sequence DTG and a sequence encoding DSG or DTG separated by 100-300
CC amino acids. When mutated the APP gene causes an autosomal dominant form
CC of Alzheimer's disease. APP localises to the cell surface membrane and
CC have a single C-terminal transmembrane domain. Proteolytic processing of
CC APP produces the amyloid beta protein, which is possibly very important
CC in Alzheimer's disease. The invention includes a nucleotide sequence
CC encoding the protease, a vector containing the nucleotide sequence, and a
CC cell line comprising the vector. Methods for screening for inhibitors of
CC beta secretase activity are also given in the invention. The human
CC aspartase protein and nucleotide sequences and the methods for
CC identifying inhibitors of the protease, are useful in the treatment of
CC and research in to Alzheimer's disease. (Updated on 06-AUG-2003 to
CC correct OS field.) (Updated on 12-SEP-2003 to standardise OS field)
XX
SQ Sequence 433 AA;

Query Match 100.0%; Score 16; DB 3; Length 433;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TQHGIRLPLRSGLGGA 16
||||||||||||||||
Db 2 TQHGIRLPLRSGLGGA 17

RESULT 14
AAU07213
ID AAU07213 standard; protein; 433 AA.
XX
AC AAU07213;
XX
DT 11-SEP-2003 (revised)
DT 24-OCT-2001 (first entry)
XX
DE T7-human aspartyl protease 2a deltaTM (low GC).
XX
KW Human; aspartyl protease 1; Asp-1; nootropic; neuroprotective;
KW aspartyl protease 2; Asp2; amyloid protein precursor; APP;
KW beta-secretase; Alzheimer's disease.
XX
OS Homo sapiens.
OS Enterobacteria phage T7.
XX
PN WO200149097-A2.
XX
PD 12-JUL-2001.
XX
PF 09-MAY-2001; 2001WO-IB000797.
XX
PR 09-MAY-2001; 2001WO-IB000797.
XX
PA (BIEN/) BIENKOWSKI M J.
PA (GURN/) GURNEY M E.
PA (HEIN/) HEINRIKSON R L.
PA (PARO/) PARODI L A.
PA (YANR/) YAN R.
XX
PI Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;
XX
DR WPI; 2001-502548/55.
DR N-PSDB; AAS11713.
XX
PT Novel purified polypeptide comprising fragment of mammalian aspartyl
PT protease 2, lacking Asp2 transmembrane domain and retaining beta
PT secretase activity of Asp2 useful for identifying inhibitors of Asp2
PT activity.
XX
PS Example 9; Fig 8; 185pp; English.
XX
CC The invention relates to a novel purified polypeptide comprising a
CC fragment of mammalian aspartyl protease 2 (Asp2) protein which lacks the
CC Asp2 transmembrane domain and the Asp2 protein, and where the polypeptide
CC and the fragment retain the beta-secretase activity of the mammalian Asp2
CC protein. Also included is an isoform of amyloid protein precursor (APP)
CC comprising the amino acid sequence of a APP or its fragment containing an
CC APP cleavage site recognisable by a mammalian beta-secretase, and further
CC comprising two lysine residues at the carboxyl terminus of the amino acid
CC sequence of the mammalian APP or APP fragment. The polypeptides are used
CC for assaying for modulators of beta-secretase activity; identifying
CC agents that inhibit the APP processing activity of human Asp2 aspartyl
CC protease (Hu-Asp2); identifying agents that modulate the activity of Asp2
CC ; and for reducing cellular production of amyloid beta (Abeta) from APP.
CC Agents identified by the above methods are useful for treating
CC Alzheimer's disease; for identifying modulators of amyloid-beta (Abeta)
CC peptide production, and for use in designing therapeutics for the
CC treatment or prevention of Alzheimer's disease. Probes and primers
CC derived from Asp nucleic acid sequences are useful for detecting Hu-Asp
CC nucleic acids in in vitro assays and in Northern and Southern blots. The
CC present sequence represents the amino acid sequence of T7-human Asp-2a
CC delta TM (low GC) construct which has a T7 tag, has the GC content of the
CC 5' sequence reduced by site-directed mutagenesis, and lacks the
CC transmembrane domain. This construct was used for bacterial expression
CC and purification of human Asp2a. (Updated on 11-SEP-2003 to standardise
CC OS field)
XX
SQ Sequence 433 AA;

Query Match 100.0%; Score 16; DB 4; Length 433;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TQHGIRLPLRSGLGGA 16
||||||||||||||||
Db 2 TQHGIRLPLRSGLGGA 17

RESULT 15
AAE10640
ID AAE10640 standard; protein; 433 AA.
XX
AC AAE10640;
XX
DT 10-DEC-2001 (first entry)
XX
DE Human-pro-Asp 2(a) protein lacking TM domain.
XX
KW Human; aspartyl protease 1; Asp1; amyloid precursor protein; APP;
KW Alzheimer's disease; AD; dementia; neurofibrillary tangle; gliosis;
KW amyloid plaque; neuronal loss; proteolytic; nootropic; neuroprotective;
KW Human-pro-Asp 2(a) protein.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN GB2357767-A.
XX
PD 04-JUL-2001.
XX
PF 22-SEP-2000; 2000GB-00023315.
XX
PR 23-SEP-1999; 99US-00404133.
PR 23-SEP-1999; 99US-0155493P.
PR 23-SEP-1999; 99WO-US020881.
PR 13-OCT-1999; 99US-00416901.
PR 06-DEC-1999; 99US-0169232P.
XX
PA (PHAA) PHARMACIA & UPJOHN CO.
XX
PI Bienkowkski MJ, Gurney M;
XX
DR WPI; 2001-444208/48.
DR N-PSDB; AAD17876.
XX
PT Polypeptide comprising fragments of human aspartyl protease with amyloid
PT precursor protein processing activity and alpha-secretase activity, for

PT identifying modulators useful in treating Alzheimer's disease.
XX
PS Example 9; Fig 8; 187pp; English.
XX
CC The patent discloses human aspartyl protease 1 (hu-Asp1) or modified Asp1
CC proteins which lack transmembrane domain or amino terminal domain or
CC cytoplasmic domain and retains alpha-secretase activity and amyloid
CC protein precursor (APP) processing activity. The proteins of the
CC invention are useful for assaying hu-Asp1 alpha-secretase activity, which
CC in turn is useful for identifying modulators of hu-Asp1 alpha-secretase
CC activity, where modulators that increase hu-Asp1 alpha-secretase activity
CC are useful for treating Alzheimer's disease (AD) which causes progressive
CC dementia with consequent formation of amyloid plaques, neurofibrillary
CC tangles, gliosis and neuronal loss. Hu-Asp1 protease substrate is useful
CC for assaying hu-Asp1 proteolytic activity, by contacting hu-Asp1 protein
CC with the substrate under acidic conditions and determining the level of
CC hu-Asp1 proteolytic activity. The present sequence human-pro-Asp 2(a)
CC protein lacking a transmembrane (TM) domain (low GC). This sequence is
CC generated from human Asp 2(a) protein by the deletion of its C-terminal
CC transmembrane domain and change of degenerate codon bases in 15 amino
CC acid positions from G/C to A/T to reduce the GC content
XX
SQ Sequence 433 AA;

Query Match 100.0%; Score 16; DB 4; Length 433;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 TQHGIRLPLRSGLGGA 16
              ||||||||||||||||
Db          2 TQHGIRLPLRSGLGGA 17
```

Search completed: July 26, 2005, 16:34:18
Job time : 168 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: July 26, 2005, 16:31:35 ; Search time 153 Seconds
(without alignments)
40.679 Million cell updates/sec

Title: US-10-726-967A-3
Perfect score: 16
Sequence: 1 TQHGIRLPLRSGLGGA 16

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1741741 seqs, 388992284 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1741741

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep:*
20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	16	100.0	16	17	US-10-726-967A-3	Sequence 3, Appli
2	16	100.0	425	15	US-10-372-473-3	Sequence 3, Appli
3	16	100.0	428	9	US-09-794-927-51	Sequence 51, Appl
4	16	100.0	428	9	US-09-795-847-51	Sequence 51, Appl
5	16	100.0	428	9	US-09-794-743-51	Sequence 51, Appl
6	16	100.0	428	9	US-09-794-748-51	Sequence 51, Appl
7	16	100.0	428	9	US-09-794-925-51	Sequence 51, Appl
8	16	100.0	428	9	US-09-681-442-51	Sequence 51, Appl
9	16	100.0	428	10	US-09-869-414-51	Sequence 51, Appl
10	16	100.0	428	10	US-09-548-366-51	Sequence 51, Appl
11	16	100.0	428	15	US-10-652-927-51	Sequence 51, Appl
12	16	100.0	428	15	US-10-652-830-51	Sequence 51, Appl
13	16	100.0	428	16	US-10-652-045-51	Sequence 51, Appl
14	16	100.0	428	16	US-10-476-935-51	Sequence 51, Appl
15	16	100.0	428	17	US-10-477-076-51	Sequence 51, Appl
16	16	100.0	432	15	US-10-372-473-2	Sequence 2, Appli
17	16	100.0	433	9	US-09-794-927-26	Sequence 26, Appl
18	16	100.0	433	9	US-09-795-847-26	Sequence 26, Appl
19	16	100.0	433	9	US-09-794-743-26	Sequence 26, Appl
20	16	100.0	433	9	US-09-794-748-26	Sequence 26, Appl
21	16	100.0	433	9	US-09-794-925-26	Sequence 26, Appl
22	16	100.0	433	9	US-09-681-442-26	Sequence 26, Appl
23	16	100.0	433	10	US-09-869-414-26	Sequence 26, Appl
24	16	100.0	433	10	US-09-548-366-26	Sequence 26, Appl
25	16	100.0	433	15	US-10-652-927-26	Sequence 26, Appl
26	16	100.0	433	15	US-10-652-830-26	Sequence 26, Appl
27	16	100.0	433	16	US-10-652-045-26	Sequence 26, Appl
28	16	100.0	433	16	US-10-476-935-26	Sequence 26, Appl
29	16	100.0	433	17	US-10-940-867-26	Sequence 26, Appl
30	16	100.0	433	17	US-10-726-967A-78	Sequence 78, Appl
31	16	100.0	433	17	US-10-726-967A-81	Sequence 81, Appl
32	16	100.0	433	17	US-10-726-967A-84	Sequence 84, Appl
33	16	100.0	433	17	US-10-477-076-26	Sequence 26, Appl
34	16	100.0	434	9	US-09-794-927-53	Sequence 53, Appl
35	16	100.0	434	9	US-09-795-847-53	Sequence 53, Appl
36	16	100.0	434	9	US-09-794-743-53	Sequence 53, Appl
37	16	100.0	434	9	US-09-794-748-53	Sequence 53, Appl
38	16	100.0	434	9	US-09-794-925-53	Sequence 53, Appl
39	16	100.0	434	9	US-09-681-442-53	Sequence 53, Appl
40	16	100.0	434	10	US-09-869-414-53	Sequence 53, Appl
41	16	100.0	434	10	US-09-548-366-53	Sequence 53, Appl
42	16	100.0	434	15	US-10-652-927-53	Sequence 53, Appl
43	16	100.0	434	15	US-10-652-830-53	Sequence 53, Appl
44	16	100.0	434	16	US-10-652-045-53	Sequence 53, Appl
45	16	100.0	434	16	US-10-476-935-53	Sequence 53, Appl

ALIGNMENTS

RESULT 1
US-10-726-967A-3
; Sequence 3, Application US/10726967A
; Publication No. US20050074456A1
; GENERAL INFORMATION:
; APPLICANT: Ballinger, Marcus
; TITLE OF INVENTION: Constructs for Homogenously Processed Preparations of Beta Site
; TITLE OF INVENTION: App-Cleaving Enzyme
; FILE REFERENCE: 2004345-0021
; CURRENT APPLICATION NUMBER: US/10/726,967A
; CURRENT FILING DATE: 2003-12-02
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Residues 22-37 of human BACE1 preprosequence
US-10-726-967A-3

Query Match 100.0%; Score 16; DB 17; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.7e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 TQHGIRLPLRSGLGGA 16
              ||||||||||||||||
Db          1 TQHGIRLPLRSGLGGA 16
```

RESULT 2
US-10-372-473-3
; Sequence 3, Application US/10372473
; Publication No. US20040005691A1

```
 ; GENERAL INFORMATION:
 ;  APPLICANT: Chou, Kuo-Chen
 ;  APPLICANT:  Howe, W. Jeffery
 ;  TITLE OF INVENTION: Modified BACE
 ;  FILE REFERENCE: MBHB 01-1766-A
 ;  CURRENT APPLICATION NUMBER: US/10/372,473
 ;  CURRENT FILING DATE:  2003-02-21
 ;  NUMBER OF SEQ ID NOS: 24
 ;  SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 3
 ;   LENGTH: 425
 ;   TYPE: PRT
 ;   ORGANISM: Homo sapiens
 ;   FEATURE:
 ;   NAME/KEY: MISC_FEATURE
 ;   OTHER INFORMATION: Human beta-secretase zymogen.
US-10-372-473-3

  Query Match             100.0%;  Score 16;  DB 15;  Length 425;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-07;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TQHGIRLPLRSGLGGA 16
              ||||||||||||||||
Db          1 TQHGIRLPLRSGLGGA 16


RESULT 3
US-09-794-927-51
; Sequence 51, Application US/09794927
; Patent No. US20010016324A1
; GENERAL INFORMATION:
;  APPLICANT:  Gurney, Mark E.
;  APPLICANT:  Bienkowski, Michael J.
;  APPLICANT:  Heinrikson, Robert L.
;  APPLICANT:  Parodi, Luis A.
;  APPLICANT:  Yan, Riqiang
;  TITLE OF INVENTION:  ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
;  TITLE OF INVENTION:  USES
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE:  28341/6280FG
;  CURRENT APPLICATION NUMBER: US/09/794,927
;  CURRENT FILING DATE:  2001-02-27
;  PRIOR APPLICATION NUMBER:  09/416,901
;  PRIOR FILING DATE:  1999-10-13
;  PRIOR APPLICATION NUMBER:  60/155,493
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  09/404,133
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  PCT/US99/20881
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  60/101,594
;  PRIOR FILING DATE:  1998-09-24
;  NUMBER OF SEQ ID NOS:  73
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 51
;   LENGTH: 428
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Hu-Asp2(b)
;   OTHER INFORMATION: delta TM
US-09-794-927-51

  Query Match             100.0%;  Score 16;  DB 9;  Length 428;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-07;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TQHGIRLPLRSGLGGA 16
              ||||||||||||||||
Db         22 TQHGIRLPLRSGLGGA 37


RESULT 4
US-09-795-847-51
; Sequence 51, Application US/09795847
; Patent No. US20010018208A1
; GENERAL INFORMATION:
;  APPLICANT:  Gurney, Mark E.
;  APPLICANT:  Bienkowski, Michael J.
;  APPLICANT:  Heinrikson, Robert L.
;  APPLICANT:  Parodi, Luis A.
;  APPLICANT:  Yan, Riqiang
;  TITLE OF INVENTION:  ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
;  TITLE OF INVENTION:  USES
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE:  28341/6280DE
;  CURRENT APPLICATION NUMBER: US/09/795,847
;  CURRENT FILING DATE:  2001-02-28
;  PRIOR APPLICATION NUMBER:  09/416,901
;  PRIOR FILING DATE:  1999-10-13
;  PRIOR APPLICATION NUMBER:  60/155,493
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  09/404,133
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  PCT/US99/20881
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  60/101,594
;  PRIOR FILING DATE:  1998-09-24
;  NUMBER OF SEQ ID NOS:  73
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 51
;   LENGTH: 428
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Hu-Asp2(b)
;   OTHER INFORMATION: delta TM
US-09-795-847-51

  Query Match             100.0%;  Score 16;  DB 9;  Length 428;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-07;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TQHGIRLPLRSGLGGA 16
              ||||||||||||||||
Db         22 TQHGIRLPLRSGLGGA 37


RESULT 5
US-09-794-743-51
; Sequence 51, Application US/09794743
; Patent No. US20010021391A1
; GENERAL INFORMATION:
;  APPLICANT:  Gurney, Mark E.
;  APPLICANT:  Bienkowski, Michael J.
;  APPLICANT:  Heinrikson, Robert L.
;  APPLICANT:  Parodi, Luis A.
;  APPLICANT:  Yan, Riqiang
;  TITLE OF INVENTION:  ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
;  TITLE OF INVENTION:  USES
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE:  28341/6280BC
;  CURRENT APPLICATION NUMBER: US/09/794,743
;  CURRENT FILING DATE:  2001-02-27
;  PRIOR APPLICATION NUMBER:  09/416,901
;  PRIOR FILING DATE:  1999-10-13
;  PRIOR APPLICATION NUMBER:  60/155,493
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  09/404,133
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  PCT/US99/20881
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  60/101,594
;  PRIOR FILING DATE:  1998-09-24
;  NUMBER OF SEQ ID NOS:  73
```

```
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 51
;   LENGTH: 428
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Hu-Asp2(b)
;   OTHER INFORMATION: delta TM
US-09-794-743-51

  Query Match             100.0%;  Score 16;  DB 9;  Length 428;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-07;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TQHGIRLPLRSGLGGA 16
              ||||||||||||||||
Db         22 TQHGIRLPLRSGLGGA 37


RESULT 6
US-09-794-748-51
; Sequence 51, Application US/09794748
; Patent No. US20020037315A1
; GENERAL INFORMATION:
;  APPLICANT:  Gurney, Mark E.
;  APPLICANT:  Bienkowski, Michael J.
;  APPLICANT:  Heinrikson, Robert L.
;  APPLICANT:  Parodi, Luis A.
;  APPLICANT:  Yan, Riqiang
;  TITLE OF INVENTION:  ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
;  TITLE OF INVENTION:  USES
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE:  28341/6280JL
;  CURRENT APPLICATION NUMBER: US/09/794,748
;  CURRENT FILING DATE:  2001-02-27
;  PRIOR APPLICATION NUMBER:  09/416,901
;  PRIOR FILING DATE:  1999-10-13
;  PRIOR APPLICATION NUMBER:  60/155,493
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  09/404,133
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  PCT/US99/20881
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  60/101,594
;  PRIOR FILING DATE:  1998-09-24
;  NUMBER OF SEQ ID NOS:  73
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 51
;   LENGTH: 428
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Hu-Asp2(b)
;   OTHER INFORMATION: delta TM
US-09-794-748-51

  Query Match             100.0%;  Score 16;  DB 9;  Length 428;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-07;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TQHGIRLPLRSGLGGA 16
              ||||||||||||||||
Db         22 TQHGIRLPLRSGLGGA 37


RESULT 7
US-09-794-925-51
; Sequence 51, Application US/09794925
; Patent No. US20020064819A1
; GENERAL INFORMATION:
;  APPLICANT:  Gurney, Mark E.
;  APPLICANT:  Bienkowski, Michael J.
;  APPLICANT:  Heinrikson, Robert L.
;  APPLICANT:  Parodi, Luis A.
;  APPLICANT:  Yan, Riqiang
;  TITLE OF INVENTION:  ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE:  28341/6280HI
;  CURRENT APPLICATION NUMBER: US/09/794,925
;  CURRENT FILING DATE:  2001-02-27
;  PRIOR APPLICATION NUMBER:  09/416,901
;  PRIOR FILING DATE:  1999-10-13
;  PRIOR APPLICATION NUMBER:  60/155,493
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  09/404,133
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  PCT/US99/20881
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  60/101,594
;  PRIOR FILING DATE:  1998-09-24
;  NUMBER OF SEQ ID NOS:  73
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 51
;   LENGTH: 428
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Hu-Asp2(b)
;   OTHER INFORMATION: delta TM
US-09-794-925-51

  Query Match             100.0%;  Score 16;  DB 9;  Length 428;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-07;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TQHGIRLPLRSGLGGA 16
              ||||||||||||||||
Db         22 TQHGIRLPLRSGLGGA 37


RESULT 8
US-09-681-442-51
; Sequence 51, Application US/09681442
; Patent No. US20020081634A1
; GENERAL INFORMATION:
;  APPLICANT: Gurney, Mark E.
;  APPLICANT:  Bienkowski, Michael J.
;  APPLICANT:  Heinrikson, Robert L.
;  APPLICANT:  Parodi, Luis A.
;  APPLICANT:  Yan, Riqiang
;  TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE: 28341/6280FG
;  CURRENT APPLICATION NUMBER: US/09/681,442
;  CURRENT FILING DATE:  2001-04-05
;  PRIOR APPLICATION NUMBER: 09/416,901
;  PRIOR FILING DATE: 1999-10-13
;  PRIOR APPLICATION NUMBER: 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 51
;   LENGTH: 428
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Hu-Asp2(b)
;   OTHER INFORMATION: delta TM
US-09-681-442-51
```

```
  Query Match           100.0%;  Score 16;  DB 9;  Length 428;
  Best Local Similarity  100.0%;  Pred. No. 2.6e-07;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TQHGIRLPLRSGLGGA 16
              ||||||||||||||||
Db         22 TQHGIRLPLRSGLGGA 37


RESULT 9
US-09-869-414-51
; Sequence 51, Application US/09869414
; Publication No. US20030077226A1
; GENERAL INFORMATION:
;  APPLICANT: Beinkowski et al.
;  TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE: 28341/6280M
;  CURRENT APPLICATION NUMBER: US/09/869,414
;  CURRENT FILING DATE:  2001-06-27
;  PRIOR APPLICATION NUMBER: 09/416,901
;  PRIOR FILING DATE: 1999-10-13
;  PRIOR APPLICATION NUMBER: 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 51
;    LENGTH: 428
;    TYPE: PRT
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Description of Artificial Sequence: Hu-Asp2(b)
;    OTHER INFORMATION: delta TM
US-09-869-414-51

  Query Match           100.0%;  Score 16;  DB 10;  Length 428;
  Best Local Similarity  100.0%;  Pred. No. 2.6e-07;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TQHGIRLPLRSGLGGA 16
              ||||||||||||||||
Db         22 TQHGIRLPLRSGLGGA 37


RESULT 10
US-09-548-366-51
; Sequence 51, Application US/09548366
; Publication No. US20030104365A1
; GENERAL INFORMATION:
;  APPLICANT:  Gurney, Mark E.
;  APPLICANT:  Bienkowski, Michael J.
;  APPLICANT:  Heinrikson, Robert L.
;  APPLICANT:  Parodi, Luis A.
;  APPLICANT:  Yan, Riqiang
;  TITLE OF INVENTION:  ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
;  TITLE OF INVENTION:  USES THEREFOR
;  FILE REFERENCE:  28341/6280A
;  CURRENT APPLICATION NUMBER: US/09/548,366
;  CURRENT FILING DATE:  2000-04-12
;  PRIOR APPLICATION NUMBER:  60/155,493
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  09/404,133
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  PCT/US99/20881
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  60/101,594
;  PRIOR FILING DATE:  1998-09-24
;  NUMBER OF SEQ ID NOS:  65
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 51
;    LENGTH: 428
;    TYPE: PRT
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Description of Artificial Sequence: Hu-Asp2(b)
;    OTHER INFORMATION: delta TM
US-09-548-366-51

  Query Match           100.0%;  Score 16;  DB 10;  Length 428;
  Best Local Similarity  100.0%;  Pred. No. 2.6e-07;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TQHGIRLPLRSGLGGA 16
              ||||||||||||||||
Db         22 TQHGIRLPLRSGLGGA 37


RESULT 11
US-10-652-927-51
; Sequence 51, Application US/10652927
; Publication No. US20040043408A1
; GENERAL INFORMATION:
;  APPLICANT: Gurney et al.
;  TITLE OF INVENTION: Alzheimer's Disease Secretase, APP Substrates Therefor and Uses
;  TITLE OF INVENTION:  Therefor
;  FILE REFERENCE: 29915/6280N3
;  CURRENT APPLICATION NUMBER: US/10/652,927
;  CURRENT FILING DATE:  2003-08-29
;  PRIOR APPLICATION NUMBER: 09/794,925
;  PRIOR FILING DATE: 2001-02-27
;  PRIOR APPLICATION NUMBER: 09/416,901
;  PRIOR FILING DATE: 1999-10-13
;  PRIOR APPLICATION NUMBER: 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 74
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 51
;    LENGTH: 428
;    TYPE: PRT
;    ORGANISM: Artificial sequence
;    FEATURE:
;    OTHER INFORMATION: Hu-Asp2(b) delta TM
US-10-652-927-51

  Query Match           100.0%;  Score 16;  DB 15;  Length 428;
  Best Local Similarity  100.0%;  Pred. No. 2.6e-07;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TQHGIRLPLRSGLGGA 16
              ||||||||||||||||
Db         22 TQHGIRLPLRSGLGGA 37


RESULT 12
US-10-652-830-51
; Sequence 51, Application US/10652830
; Publication No. US20040048303A1
; GENERAL INFORMATION:
;  APPLICANT: Gurney et al.
;  TITLE OF INVENTION: Alzheimer's Disease Secretase, APP Substrates Therefor and Uses
;  TITLE OF INVENTION:  Therefor
;  FILE REFERENCE: 29915/6280N1
;  CURRENT APPLICATION NUMBER: US/10/652,830
;  CURRENT FILING DATE:  2003-08-29
```

```
;  PRIOR APPLICATION NUMBER: 09/794,925
;  PRIOR FILING DATE: 2001-02-27
;  PRIOR APPLICATION NUMBER: 09/416,901
;  PRIOR FILING DATE: 1999-10-13
;  PRIOR APPLICATION NUMBER: 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 74
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 51
;    LENGTH: 428
;    TYPE: PRT
;    ORGANISM: Artificial sequence
;    FEATURE:
;    OTHER INFORMATION: Hu-Asp2(b) delta TM
US-10-652-830-51

  Query Match             100.0%;  Score 16;  DB 15;  Length 428;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-07;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TQHGIRLPLRSGLGGA 16
              ||||||||||||||||
Db         22 TQHGIRLPLRSGLGGA 37


RESULT 13
US-10-652-045-51
; Sequence 51, Application US/10652045
; Publication No. US20040166507A1
; GENERAL INFORMATION:
;  APPLICANT: Gurney et al.
;  TITLE OF INVENTION: Alzheimer's Disease Secretase, APP Substrates Therefor and Uses
;  TITLE OF INVENTION:  Therefor
;  FILE REFERENCE: 29915/6280N2
;  CURRENT APPLICATION NUMBER: US/10/652,045
;  CURRENT FILING DATE:  2003-08-29
;  PRIOR APPLICATION NUMBER: 09/794,925
;  PRIOR FILING DATE: 2001-02-27
;  PRIOR APPLICATION NUMBER: 09/416,901
;  PRIOR FILING DATE: 1999-10-13
;  PRIOR APPLICATION NUMBER: 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 74
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 51
;    LENGTH: 428
;    TYPE: PRT
;    ORGANISM: Artificial sequence
;    FEATURE:
;    OTHER INFORMATION: Hu-Asp2(b) delta TM
US-10-652-045-51

  Query Match             100.0%;  Score 16;  DB 16;  Length 428;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-07;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TQHGIRLPLRSGLGGA 16
              ||||||||||||||||
Db         22 TQHGIRLPLRSGLGGA 37


RESULT 14
US-10-476-935-51
; Sequence 51, Application US/10476935
; Publication No. US20040234976A1
; GENERAL INFORMATION:
;  APPLICANT: Beinkowski et al.
;  TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE: 28341/6280M1
;  CURRENT APPLICATION NUMBER: US/10/476,935
;  CURRENT FILING DATE:  2003-11-06
;  PRIOR APPLICATION NUMBER: 09/416,901
;  PRIOR FILING DATE: 1999-10-13
;  PRIOR APPLICATION NUMBER: 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 51
;    LENGTH: 428
;    TYPE: PRT
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Description of Artificial Sequence: Hu-Asp2(b)
;    OTHER INFORMATION: delta TM
US-10-476-935-51

  Query Match             100.0%;  Score 16;  DB 16;  Length 428;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-07;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TQHGIRLPLRSGLGGA 16
              ||||||||||||||||
Db         22 TQHGIRLPLRSGLGGA 37


RESULT 15
US-10-477-076-51
; Sequence 51, Application US/10477076
; Publication No. US20050080232A1
; GENERAL INFORMATION:
;  APPLICANT: Beinkowski et al.
;  TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE: 28341/6280M2
;  CURRENT APPLICATION NUMBER: US/10/477,076
;  CURRENT FILING DATE:  2003-11-06
;  PRIOR APPLICATION NUMBER: 09/416,901
;  PRIOR FILING DATE: 1999-10-13
;  PRIOR APPLICATION NUMBER: 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 51
;    LENGTH: 428
;    TYPE: PRT
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Description of Artificial Sequence: Hu-Asp2(b)
;    OTHER INFORMATION: delta TM
US-10-477-076-51
```

Query Match 100.0%; Score 16; DB 17; Length 428;
Best Local Similarity 100.0%; Pred. No. 2.6e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 TQHGIRLPLRSGLGGA 16
              ||||||||||||||||
Db         22 TQHGIRLPLRSGLGGA 37
```

Search completed: July 26, 2005, 16:41:29
Job time : 154 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: July 26, 2005, 16:28:04 ; Search time 39 Seconds
(without alignments)
39.474 Million cell updates/sec

Title: US-10-726-967A-3
Perfect score: 16
Sequence: 1 TQHGIRLPLRSGLGGA 16

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	16	100.0	501	2	A59090	aspartic proteinas
2	7	43.8	125	2	E81814	hypothetical prote
3	7	43.8	239	2	AG0420	phosphonates trans
4	7	43.8	259	2	A75547	hypothetical prote
5	7	43.8	352	2	D64966	membrane protein y
6	6	37.5	157	2	AG2675	hypothetical prote
7	6	37.5	169	2	E90983	probable GDP-L-fuc
8	6	37.5	169	2	H85828	GDP-mannose mannos
9	6	37.5	225	2	D81813	hypothetical prote
10	6	37.5	237	2	T35108	hypothetical prote
11	6	37.5	241	2	T26676	hypothetical prote
12	6	37.5	246	2	AG3644	flagellar biosynth
13	6	37.5	252	2	AE3631	nitrous-oxide redu
14	6	37.5	274	2	D97653	hypothetical prote
15	6	37.5	274	2	AB2877	conserved hypothet
16	6	37.5	284	2	B41224	homeotic protein p
17	6	37.5	292	2	C83520	dihydrodipicolinat
18	6	37.5	299	2	B95149	heat shock protein
19	6	37.5	302	2	A99017	heat shock protein
20	6	37.5	325	2	A72724	hypothetical prote
21	6	37.5	338	2	AE3334	metal chelate tran
22	6	37.5	352	2	T02875	ribosomal protein
23	6	37.5	352	2	D85826	probable transport
24	6	37.5	352	2	G90980	probable transport
25	6	37.5	379	2	A57477	potassium channel
26	6	37.5	390	2	AF3425	oxidoreductase (EC
27	6	37.5	399	2	AC2785	MFS permease [drug
28	6	37.5	399	2	D97564	hypothetical prote
29	6	37.5	411	2	T34585	probable secreted
30	6	37.5	416	2	T32458	hypothetical prote
31	6	37.5	423	2	A45363	somatoliberin rece
32	6	37.5	430	2	A84165	UDP-glucose dehydr
33	6	37.5	430	2	D96536	hypothetical prote
34	6	37.5	437	2	AB0151	conserved hypothet
35	6	37.5	439	2	D70954	hypothetical glyci
36	6	37.5	444	2	E65045	hypothetical prote
37	6	37.5	444	2	C85913	hypothetical prote
38	6	37.5	444	2	A91069	hypothetical prote
39	6	37.5	451	2	I46586	growth hormone-rel
40	6	37.5	454	2	H83377	probable transport
41	6	37.5	463	2	G83175	probable metallo-o
42	6	37.5	464	2	S29754	growth hormone-rel
43	6	37.5	504	2	AD3629	vdcC protein [impo
44	6	37.5	518	2	S75811	gamma-glutamyltran
45	6	37.5	525	2	AF2950	GGDEF family prote

ALIGNMENTS

RESULT 1
A59090
aspartic proteinase (EC 3.4.23.-) BACE precursor - human
N;Alternate names: beta-secretase; beta-site APP cleaving enzyme
C;Species: Homo sapiens (man)
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: A59090
R;Vassar, R.; Bennett, B.D.; Babu-Khan, S.; Kahn, S.; Mendiaz, E.A.; Denis, P.; Teplow, M.A.; Biere, A.L.; Curran, E.; Burgess, T.; Louis, J.C.; Collins, F.; Treanor, J.; Roger
Science 286, 735-741, 1999
A;Title: beta-Secretase cleavage of Alzheimer's amyloid precursor protein by the transme
A;Reference number: A59090; MUID:20002972; PMID:10531052
A;Note: submitted to GenBank, September 1999
A;Accession: A59090
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-501 <VAS>
A;Cross-references: UNIPROT:P56817; GB:AF190725; NID:g6118538; PIDN:AAF04142.1; PID:g611
C;Genetics:
A;Gene: BACE
C;Superfamily: beta-secretase
C;Keywords: Alzheimer's disease; aspartic proteinase; brain; glycoprotein; hydrolase; pi
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-45/Domain: propeptide #status predicted <PRO>
F;46-501/Product: acid proteinase BACE #status predicted <MAT>
F;461-477/Domain: transmembrane #status predicted <TRN>
F;93,289/Active site: Asp #status predicted
F;153,172,223,354/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;330-380/Disulfide bonds: #status predicted

Query Match 100.0%; Score 16; DB 2; Length 501;
Best Local Similarity 100.0%; Pred. No. 1.8e-09;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 TQHGIRLPLRSGLGGA 16
              ||||||||||||||||
Db         22 TQHGIRLPLRSGLGGA 37
```

RESULT 2
E81814
hypothetical protein NMA1874 [imported] - Neisseria meningitidis (strain Z2491 serogrou
C;Species: Neisseria meningitidis
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
C;Accession: E81814
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis Z2491.
A;Reference number: A81775; MUID:20222556; PMID:10761919
A;Accession: E81814
A;Status: preliminary

A;Molecule type: DNA
A;Residues: 1-125 <PAR>
A;Cross-references: UNIPROT:Q9JTC5; GB:AL162757; GB:AL157959; NID:g7380371; PIDN:CAB8509
A;Experimental source: serogroup A, strain Z2491
C;Genetics:
A;Gene: NMA1874
C;Superfamily: Neisseria meningitidis hypothetical protein NMA1874

Query Match 43.8%; Score 7; DB 2; Length 125;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 LRSGLGG 15
|||||||
Db 109 LRSGLGG 115

RESULT 3
AG0420
phosphonates transport ATP-binding protein phnL [imported] - Yersinia pestis (strain CO9
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AG0420
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AG0420
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-239 <KUR>
A;Cross-references: UNIPROT:Q8ZBF4; GB:AL590842; PIDN:CAC92691.1; PID:g15981386; GSPDB:G
C;Genetics:
A;Gene: phnL
C;Superfamily: short-chain ATP-binding cassette proteins; ATP-binding cassette homology

Query Match 43.8%; Score 7; DB 2; Length 239;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QHGIRLP 8
|||||||
Db 20 QHGIRLP 26

RESULT 4
A75547
hypothetical protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: A75547
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: A75547
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-259 <WHI>
A;Cross-references: UNIPROT:Q9RXU2; GB:AE001883; GB:AE000513; NID:g6457878; PIDN:AAF0980
A;Experimental source: strain R1
C;Genetics:
A;Gene: DR0214
A;Map position: 1
C;Superfamily: Deinococcus radiodurans hypothetical protein DR0214

Query Match 43.8%; Score 7; DB 2; Length 259;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 HGIRLPL 9
|||||||
Db 190 HGIRLPL 196

RESULT 5
D64966
membrane protein yeeE - Escherichia coli (strain K-12)
C;Species: Escherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
C;Accession: D64966
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: D64966
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-352 <BLAT>
A;Cross-references: UNIPROT:P33015; GB:AE000292; GB:U00096; NID:g1788310; PIDN:AAC75074.1
A;Experimental source: strain K-12, substrain MG1655
C;Genetics:
A;Gene: yeeE
C;Keywords: transmembrane protein
F;2-18/Domain: transmembrane #status predicted <TM1>
F;44-60/Domain: transmembrane #status predicted <TM2>
F;75-91/Domain: transmembrane #status predicted <TM3>
F;106-122/Domain: transmembrane #status predicted <TM4>
F;153-169/Domain: transmembrane #status predicted <TM5>
F;201-217/Domain: transmembrane #status predicted <TM6>
F;250-266/Domain: transmembrane #status predicted <TM7>
F;320-336/Domain: transmembrane #status predicted <TM8>

Query Match 43.8%; Score 7; DB 2; Length 352;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 LRSGLGG 15
|||||||
Db 283 LRSGLGG 289

RESULT 6
AG2675
hypothetical protein Atu0805 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Accession: AG2675
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L
erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AG2675
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-157 <KUR>
A;Cross-references: UNIPROT:Q8UH78; GB:AE008688; PIDN:AAL41821.1; PID:g17739178; GSPDB:GI
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: Atu0805
A;Map position: circular chromosome

Query Match 37.5%; Score 6; DB 2; Length 157;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PLRSGL 13

```
              ||||||
Db         81 PLRSGL 86


RESULT 7
E90983
probable GDP-L-fucose pathway enzyme [imported] - Escherichia coli (strain O157:H7, subs
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 16-Aug-2004
C;Accession: E90983
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: E90983
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-169 <HAY>
A;Cross-references: UNIPROT:O85341; GB:BA000007; PIDN:BAB36260.1; PID:g13362305; GSPDB:G
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: ECs2837
C;Superfamily: mutT domain homology

  Query Match             37.5%;  Score 6;  DB 2;  Length 169;
  Best Local Similarity   100.0%;  Pred. No. 27;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 GIRLPL 9
              ||||||
Db         71 GIRLPL 76


RESULT 8
H85828
GDP-mannose mannosylhydrolase [imported] - Escherichia coli (strain O157:H7, substrain E
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Aug-2004
C;Accession: H85828
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: H85828
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-169 <STO>
A;Cross-references: UNIPROT:O85341; GB:AE005174; NID:g12516220; PIDN:AAG57092.1; GSPDB:G
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: wbdQ
C;Superfamily: mutT domain homology

  Query Match             37.5%;  Score 6;  DB 2;  Length 169;
  Best Local Similarity   100.0%;  Pred. No. 27;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 GIRLPL 9
              ||||||
Db         71 GIRLPL 76


RESULT 9
D81813
hypothetical protein NMA1865 [imported] - Neisseria meningitidis (strain Z2491 serogroup
C;Species: Neisseria meningitidis
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
C;Accession: D81813
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis Z2491.
A;Reference number: A81775; MUID:20222556; PMID:10761919
A;Accession: D81813
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-225 <PAR>
A;Cross-references: UNIPROT:Q9JR68; GB:AL162757; GB:AL157959; NID:g7380371; PIDN:CAB8508
A;Experimental source: serogroup A, strain Z2491
C;Genetics:
A;Gene: NMA1865

  Query Match             37.5%;  Score 6;  DB 2;  Length 225;
  Best Local Similarity   100.0%;  Pred. No. 35;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 GIRLPL 9
              ||||||
Db        197 GIRLPL 202


RESULT 10
T35108
hypothetical protein SC4H2.09 SC4H2.09 - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
C;Accession: T35108
R;Seeger, K.J.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, March 1998
A;Reference number: Z21568
A;Accession: T35108
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-237 <SEE>
A;Cross-references: UNIPROT:O69964; EMBL:AL022268; PIDN:CAA18325.1; GSPDB:GN00070; SCOED
A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: SCOEDB:SC4H2.09
C;Superfamily: Streptomyces coelicolor hypothetical protein SC4H2.09

  Query Match             37.5%;  Score 6;  DB 2;  Length 237;
  Best Local Similarity   100.0%;  Pred. No. 37;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         11 SGLGGA 16
              ||||||
Db        214 SGLGGA 219


RESULT 11
T26676
hypothetical protein Y38F1A.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T26676
R;Wallis, J.
submitted to the EMBL Data Library, October 1998
A;Reference number: Z20253
A;Accession: T26676
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-241 <WIL>
A;Cross-references: UNIPROT:Q9XWM5; EMBL:AL032639; PIDN:CAA21628.1; GSPDB:GN00020; CESP:
A;Experimental source: clone Y38F1A
C;Genetics:
A;Gene: CESP:Y38F1A.1
A;Map position: 2
A;Introns: 37/3; 76/2; 130/3; 202/3

  Query Match             37.5%;  Score 6;  DB 2;  Length 241;
  Best Local Similarity   100.0%;  Pred. No. 37;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         11 SGLGGA 16
```

```
              ||||||
Db        101 SGLGGA 106


RESULT 12
AG3644
flagellar biosynthetic protein fliP [imported] - Brucella melitensis (strain 16M)
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Accession: AG3644
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
A;Reference number: AD3252; PMID:11756688
A;Accession: AG3644
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-246 <KUR>
A;Cross-references: UNIPROT:Q8YB21; GB:AE008918; PIDN:AAL54322.1; PID:g17985302; GSPDB:G
A;Experimental source: strain 16M
C;Genetics:
A;Gene: BMEII1080
A;Map position: II
C;Superfamily: flagellar biosynthetic protein fliP

  Query Match             37.5%;  Score 6;  DB 2;  Length 246;
  Best Local Similarity   100.0%;  Pred. No. 38;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 LRSGLG 14
              ||||||
Db         75 LRSGLG 80


RESULT 13
AE3631
nitrous-oxide reductase (EC 1.7.99.6) [imported] - Brucella melitensis (strain 16M)
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Accession: AE3631
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
A;Reference number: AD3252; PMID:11756688
A;Accession: AE3631
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-252 <KUR>
A;Cross-references: UNIPROT:Q8YBC6; GB:AE008918; PIDN:AAL54216.1; PID:g17985186; GSPDB:G
A;Experimental source: strain 16M
C;Genetics:
A;Gene: BMEII0974
A;Map position: II
C;Keywords: oxidoreductase

  Query Match             37.5%;  Score 6;  DB 2;  Length 252;
  Best Local Similarity   100.0%;  Pred. No. 39;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         11 SGLGGA 16
              ||||||
Db         28 SGLGGA 33


RESULT 14
D97653
hypothetical protein AGR_C_4436 [imported] - Agrobacterium tumefaciens (strain C58, Cere
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C;Accession: D97653
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
 A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tume
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: D97653
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-274 <KUR>
A;Cross-references: UNIPROT:Q8UCN9; GB:AE007869; PIDN:AAK88181.1; PID:g15157627; GSPDB:GN
C;Genetics:
A;Gene: AGR_C_4436
A;Map position: circular chromosome

  Query Match             37.5%;  Score 6;  DB 2;  Length 274;
  Best Local Similarity   100.0%;  Pred. No. 42;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 RSGLGG 15
              ||||||
Db        249 RSGLGG 254


RESULT 15
AB2877
conserved hypothetical protein Atu2444 [imported] - Agrobacterium tumefaciens (strain C58
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Accession: AB2877
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L
erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClella
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AB2877
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-274 <KUR>
A;Cross-references: UNIPROT:Q8UCN9; GB:AE008688; PIDN:AAL43432.1; PID:g17740934; GSPDB:GI
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: Atu2444
A;Map position: circular chromosome

  Query Match             37.5%;  Score 6;  DB 2;  Length 274;
  Best Local Similarity   100.0%;  Pred. No. 42;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 RSGLGG 15
              ||||||
Db        249 RSGLGG 254


Search completed: July 26, 2005, 16:38:03
Job time : 41 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: July 26, 2005, 16:27:19 ; Search time 173 Seconds
(without alignments)
47.360 Million cell updates/sec

Title: US-10-726-967A-3
Perfect score: 16
Sequence: 1 TQHGIRLPLRSGLGGA 16

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1612378 seqs, 512079187 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	16	100.0	127	2	Q76KP0	Q76kp0 homo sapien
2	16	100.0	501	1	BAE1_HUMAN	P56817 homo sapien
3	16	100.0	501	2	Q8IYC8	Q8iyc8 homo sapien
4	10	62.5	467	2	Q8C4F4	Q8c4f4 mus musculu
5	10	62.5	501	1	BAE1_MOUSE	P56818 mus musculu
6	10	62.5	501	1	BAE1_RAT	P56819 r beta-secr
7	10	62.5	501	2	Q8BQY4	Q8bqy4 mus musculu
8	10	62.5	501	2	Q8C7R1	Q8c7r1 mus musculu
9	8	50.0	814	2	Q7SZI8	Q7szi8 oryzias lat
10	7	43.8	97	2	Q9JPF6	Q9jpf6 neisseria m
11	7	43.8	125	2	Q9JTC5	Q9jtc5 neisseria m
12	7	43.8	181	2	Q7NTK4	Q7ntk4 chromobacte
13	7	43.8	239	2	Q66F29	Q66f29 yersinia ps
14	7	43.8	239	2	Q8ZBF4	Q8zbf4 yersinia pe
15	7	43.8	259	2	Q9RXU2	Q9rxu2 deinococcus
16	7	43.8	272	2	Q67QZ3	Q67qz3 symbiobacte
17	7	43.8	293	2	Q74X41	Q74x41 yersinia pe
18	7	43.8	299	2	Q93HS7	Q93hs7 bradyrhizob
19	7	43.8	304	2	Q7SFA9	Q7sfa9 neurospora
20	7	43.8	329	2	Q7NT07	Q7nt07 chromobacte
21	7	43.8	350	2	Q93F54	Q93f54 pseudomonas
22	7	43.8	352	1	YEEE_ECOLI	P33015 escherichia
23	7	43.8	352	2	Q93F48	Q93f48 pseudomonas
24	7	43.8	352	2	Q93F55	Q93f55 pseudomonas
25	7	43.8	352	2	Q93F57	Q93f57 pseudomonas
26	7	43.8	352	2	Q93F60	Q93f60 pseudomonas
27	7	43.8	352	2	Q83R10	Q83r10 shigella fl
28	7	43.8	353	2	Q93F51	Q93f51 pseudomonas
29	7	43.8	354	2	Q93F52	Q93f52 pseudomonas
30	7	43.8	354	2	Q93F61	Q93f61 pseudomonas
31	7	43.8	457	2	Q886W9	Q886w9 pseudomonas
32	7	43.8	460	2	Q9X3V2	Q9x3v2 pseudomonas
33	7	43.8	468	2	Q88P19	Q88p19 pseudomonas
34	7	43.8	629	2	Q67QI5	Q67qi5 symbiobacte
35	7	43.8	889	2	O42723	O42723 emericella
36	7	43.8	911	1	CAFA_MOUSE	Q9qwf0 mus musculu
37	7	43.8	1104	2	Q9FU60	Q9fu60 oryza sativ
38	6	37.5	55	2	Q8PKC1	Q8pkc1 xanthomonas
39	6	37.5	55	2	Q7UVP1	Q7uvp1 rhodopirell
40	6	37.5	61	2	Q7S3N8	Q7s3n8 neurospora
41	6	37.5	68	2	Q62JX9	Q62jx9 burkholderi
42	6	37.5	77	2	Q74ET6	Q74et6 geobacter s
43	6	37.5	99	2	Q949C5	Q949c5 oryza sativ
44	6	37.5	99	2	Q6H7G5	Q6h7g5 oryza sativ
45	6	37.5	100	2	Q6ZB08	Q6zb08 oryza sativ

ALIGNMENTS

RESULT 1
Q76KP0
ID Q76KP0 PRELIMINARY; PRT; 127 AA.
AC Q76KP0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Beta-site APP cleaving enzyme isoform I-127.
GN Name=BACE;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tanahashi H.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
CC -!- SIMILARITY: Belongs to peptidase family A1.
DR EMBL; AB089958; BAC81826.1; -.
DR HSSP; P00797; 1BBS.
DR GO; GO:0009049; F:aspartic-type signal peptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001461; Peptidase_A1.
DR InterPro; IPR009119; Pept_A1_BACE.
DR InterPro; IPR009120; Pept_A1_BACE1.
DR InterPro; IPR009007; Pept_Aspartic.
DR InterPro; IPR001969; Pept_Asp_AS.
DR Pfam; PF00026; Asp; 1.
DR PRINTS; PR01816; BACE1.
DR PRINTS; PR01815; BACEFAMILY.
DR PROSITE; PS00141; ASP_PROTEASE; 1.
KW Aspartyl protease; Hydrolase; Protease.
SQ SEQUENCE 127 AA; 13939 MW; C657354CBEE72DC4 CRC64;

Query Match 100.0%; Score 16; DB 2; Length 127;
Best Local Similarity 100.0%; Pred. No. 1.3e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 TQHGIRLPLRSGLGGA 16
              ||||||||||||||||
Db         22 TQHGIRLPLRSGLGGA 37
```

RESULT 2
BAE1_HUMAN
ID BAE1_HUMAN STANDARD; PRT; 501 AA.
AC P56817; Q9BYB9; Q9BYC0; Q9BYC1; Q9UJT5;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Beta-secretase 1 precursor (EC 3.4.23.46) (Beta-site APP cleaving
DE enzyme 1) (Beta-site amyloid precursor protein cleaving enzyme 1)
DE (Aspartyl protease 2) (Asp 2) (ASP2) (Membrane-associated aspartic
DE protease 2) (Memapsin-2).

GN Name=BACE1; Synonyms=BACE;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM A).
RC TISSUE=Brain;
RX MEDLINE=20002972; PubMed=10531052; DOI=10.1126/science.286.5440.735;
RA Vassar R., Bennett B.D., Babu-Khan S., Kahn S., Mendiaz E.A.,
RA Denis P., Teplow D.B., Ross S., Amarante P., Loeloff R., Luo Y.,
RA Fisher S., Fuller J., Edenson S., Lile J., Jarosinski M.A.,
RA Biere A.L., Curran E., Burgess T., Louis J.-C., Collins F.,
RA Treanor J., Rogers G., Citron M.;
RT "Beta-secretase cleavage of Alzheimer's amyloid precursor protein by
RT the transmembrane aspartic protease BACE.";
RL Science 286:735-741(1999).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM A), SEQUENCE OF 46-68, AND
RP CHARACTERIZATION.
RC TISSUE=Brain;
RX MEDLINE=20057171; PubMed=10591214; DOI=10.1038/990114;
RA Sinha S., Anderson J.P., Barbour R., Basi G.S., Caccavello R.,
RA Davis D., Doan M., Dovey H.F., Frigon N., Hong J., Jacobson-Croak K.,
RA Jewett N., Keim P., Knops J., Lieberburg I., Power M., Tan H.,
RA Tatsuno G., Tung J., Schenk D., Seubert P., Suomensaari S.M., Wang S.,
RA Walker D., Zhao J., McConlogue L., Varghese J.;
RT "Purification and cloning of amyloid precursor protein beta-secretase
RT from human brain.";
RL Nature 402:537-540(1999).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM A).
RX MEDLINE=20057170; PubMed=10591213; DOI=10.1038/990107;
RA Yan R., Bienkowski M.J., Shuck M.E., Miao H., Tory M.C., Pauley A.M.,
RA Brashier J.R., Stratman N.C., Mathews W.R., Buhl A.E., Carter D.B.,
RA Tomasselli A.G., Parodi L.A., Heinrikson R.L., Gurney M.E.;
RT "Membrane-anchored aspartyl protease with Alzheimer's disease beta-
RT secretase activity.";
RL Nature 402:533-537(1999).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM A).
RX MEDLINE=20120043; PubMed=10656250; DOI=10.1006/mcne.1999.0811;
RA Hussain I., Powell D.J., Howlett D.R., Tew D.G., Meek T.D.,
RA Chapman C., Gloger I.S., Murphy K.E., Southan C.D., Ryan D.M.,
RA Smith T.S., Simmons D.L., Walsh F.S., Dingwall C., Christie G.;
RT "Identification of a novel aspartic proteinase (Asp 2) as beta-
RT secretase.";
RL Mol. Cell. Neurosci. 14:419-427(1999).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM B).
RC TISSUE=Brain, and Pancreas;
RA Michel B., De Pietri Tonelli D., Zacchetti D., Keller P.;
RT "New beta-site APP cleaving enzyme isoform (BACE-1B) obtained from
RT human brain and pancreas.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
RN [6]
RP SEQUENCE FROM N.A. (ISOFORM C).
RC TISSUE=Pancreas;
RA Zacchetti D., De Pietri Tonelli D., Schnurbus R.;
RT "New beta-site APP cleaving enzyme isoform (BACE-1C) obtained from
RT human pancreas.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
RN [7]
RP SEQUENCE FROM N.A. (ISOFORMS B; C AND D).
RC TISSUE=Brain;
RX MEDLINE=21408467; PubMed=11516562; DOI=10.1016/S0304-3940(01)01912-7;
RA Tanahashi H., Tabira T.;
RT "Three novel alternatively spliced isoforms of the human beta-site
RT amyloid precursor protein cleaving enzyme (BACE) and their effect on
RT amyloid beta-peptide production.";
RL Neurosci. Lett. 307:9-12(2001).
RN [8]
RP SEQUENCE OF 14-501 FROM N.A. (ISOFORM A), AND CHARACTERIZATION.
RX MEDLINE=20144060; PubMed=10677483; DOI=10.1073/pnas.97.4.1456;
RA Lin X., Koelsch G., Wu S., Downs D., Dashti A., Tang J.;
RT "Human aspartic protease memapsin 2 cleaves the beta-secretase site of
RT beta-amyloid precursor protein.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:1456-1460(2000).
RN [9]
RP DISULFIDE BONDS.
RX MEDLINE=21950860; PubMed=11953458;
RA Fischer F., Molinari M., Bodendorf U., Paganetti P.;
RT "The disulphide bonds in the catalytic domain of BACE are critical but
RT not essential for amyloid precursor protein processing activity.";
RL J. Neurochem. 80:1079-1088(2002).
CC -!- FUNCTION: Responsible for the proteolytic processing of the
CC amyloid precursor protein (APP). Cleaves at the amino terminus of
CC the A-beta peptide sequence, between residues 671 and 672 of APP,
CC leads to the generation and extracellular release of beta-cleaved
CC soluble APP, and a corresponding cell-associated carboxy-terminal
CC fragment which is later released by gamma-secretase.
CC -!- CATALYTIC ACTIVITY: Broad endopeptidase specificity. Cleaves Glu-
CC Val-Asn-Leu-|-Asp-Ala-Glu-Phe in the Swedish variant of
CC Alzheimer's amyloid precursor protein.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;
CC Name=A; Synonyms=BACE-1A, BAC-501;
CC IsoId=P56817-1; Sequence=Displayed;
CC Name=B; Synonyms=BACE-1B, BACE-I-476;
CC IsoId=P56817-2; Sequence=VSP_005223;
CC Name=C; Synonyms=BACE-1C, BACE-I-457;
CC IsoId=P56817-3; Sequence=VSP_005222;
CC Name=D; Synonyms=BACE-1D, BACE-I-432;
CC IsoId=P56817-4; Sequence=VSP_005222, VSP_005223;
CC -!- TISSUE SPECIFICITY: Brain.
CC -!- SIMILARITY: Belongs to the peptidase A1 family.
CC --

CC --
DR EMBL; AF190725; AAF04142.1; -.
DR EMBL; AF201468; AAF18982.1; -.
DR EMBL; AF200343; AAF17079.1; -.
DR EMBL; AF204943; AAF26367.1; -.
DR EMBL; AF338816; AAK38374.1; -.
DR EMBL; AF338817; AAK38375.1; -.
DR EMBL; AB050436; BAB40931.1; -.
DR EMBL; AB050437; BAB40932.1; -.
DR EMBL; AB050438; BAB40933.1; -.
DR EMBL; AF200193; AAF13715.1; -.
DR PIR; A59090; A59090.
DR PDB; 1FKN; X-ray; A/B=56-446.
DR PDB; 1M4H; X-ray; A/B=56-446.
DR MEROPS; A01.004; -.
DR Genew; HGNC:933; BACE1.
DR H-InvDB; HIX0010165; -.
DR MIM; 604252; -.
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0008798; F:beta-aspartyl-peptidase activity; TAS.
DR GO; GO:0006508; P:proteolysis and peptidolysis; TAS.
DR InterPro; IPR009119; Pept_A1_BACE.
DR InterPro; IPR009120; Pept_A1_BACE1.
DR InterPro; IPR001969; Pept_Asp_AS.
DR InterPro; IPR009007; Pept_Aspartic.
DR InterPro; IPR001461; Peptidase_A1.
DR Pfam; PF00026; Asp; 1.
DR PRINTS; PR01816; BACE1.
DR PRINTS; PR01815; BACEFAMILY.
DR PRINTS; PR00792; PEPSIN.
DR PROSITE; PS00141; ASP_PROTEASE; 1.

```
KW   3D-structure; Alternative splicing; Aspartyl protease;
KW   Direct protein sequencing; Glycoprotein; Hydrolase; Signal;
KW   Transmembrane; Zymogen.
FT   SIGNAL        1     21       Potential.
FT   PROPEP       22     45
FT   CHAIN        46    501       Beta-secretase 1.
FT   DOMAIN       22    457       Extracellular (Potential).
FT   TRANSMEM    458    478       Potential.
FT   DOMAIN      479    501       Cytoplasmic (Potential).
FT   ACT_SITE     93     93       By similarity.
FT   ACT_SITE    289    289       By similarity.
FT   DISULFID    216    420
FT   DISULFID    278    443
FT   DISULFID    330    380
FT   CARBOHYD    153    153       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    172    172       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    223    223       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    354    354       N-linked (GlcNAc. . .) (Potential).
FT   VARSPLIC    146    189       Missing (in isoform C and isoform D).
FT                                /FTId=VSP_005222.
FT   VARSPLIC    190    214       Missing (in isoform B and isoform D).
FT                                /FTId=VSP_005223.
FT   HELIX        61     63
FT   TURN         64     65
FT   STRAND       67     70
FT   TURN         71     73
FT   STRAND       74     81
FT   TURN         82     85
FT   STRAND       86     93
FT   TURN         94     95
FT   STRAND       99    102
FT   TURN        107    108
FT   HELIX       115    117
FT   TURN        119    120
FT   STRAND      122    131
FT   STRAND      136    147
FT   TURN        149    150
FT   STRAND      155    167
FT   TURN        172    173
FT   STRAND      178    181
FT   HELIX       185    187
FT   TURN        192    193
FT   HELIX       197    204
FT   STRAND      211    215
FT   HELIX       224    229

  Query Match             100.0%;  Score 16;  DB 1;  Length 501;
  Best Local Similarity   100.0%;  Pred. No. 4.2e-08;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TQHGIRLPLRSGLGGA 16
              ||||||||||||||||
Db         22 TQHGIRLPLRSGLGGA 37


RESULT 3
Q8IYC8
ID   Q8IYC8      PRELIMINARY;      PRT;   501 AA.
AC   Q8IYC8;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Beta-site APP-cleaving enzyme 1, isoform A preproprotein.
GN   Name=BACE1;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Strausberg R.;
RL   Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to peptidase family A1.
DR   EMBL; BC036084; AAH36084.1; -.
DR   HSSP; P56817; 1FKN.
DR   GO; GO:0005768; C:endosome; ISS.
DR   GO; GO:0005794; C:Golgi apparatus; ISS.
DR   GO; GO:0016021; C:integral to membrane; ISS.
DR   GO; GO:0004190; F:aspartic-type endopeptidase activity; ISS.
DR   GO; GO:0050435; P:beta-amyloid metabolism; ISS.
DR   GO; GO:0006509; P:membrane protein ectodomain proteolysis; ISS.
DR   InterPro; IPR001461; Peptidase_A1.
DR   InterPro; IPR009119; Pept_A1_BACE.
DR   InterPro; IPR009120; Pept_A1_BACE1.
DR   InterPro; IPR009007; Pept_Aspartic.
DR   InterPro; IPR001969; Pept_Asp_AS.
DR   PRINTS; PR01816; BACE1.
DR   PRINTS; PR01815; BACEFAMILY.
DR   PRINTS; PR00792; PEPSIN.
DR   PROSITE; PS00141; ASP_PROTEASE; 1.
KW   Aspartyl protease; Hydrolase; Protease.
SQ   SEQUENCE   501 AA;  55823 MW;  768595CF5517EFB7 CRC64;

  Query Match             100.0%;  Score 16;  DB 2;  Length 501;
  Best Local Similarity   100.0%;  Pred. No. 4.2e-08;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TQHGIRLPLRSGLGGA 16
              ||||||||||||||||
Db         22 TQHGIRLPLRSGLGGA 37


RESULT 4
Q8C4F4
ID   Q8C4F4      PRELIMINARY;      PRT;   467 AA.
AC   Q8C4F4;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Mus musculus 0 day neonate cerebellum cDNA, RIKEN full-length enriched
DE   library, clone:C230037E16 product:beta-site APP cleaving enzyme, full
DE   insert sequence.
GN   Name=Bace1; Synonyms=Bace;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
```

```
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Meth. Enzymol. 303:19-44(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   RIKEN FANTOM Consortium;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Cerebellum;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [6]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Cerebellum;
RA   Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA   Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA   Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA   Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA   Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA   Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA   Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA   Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA   Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA   Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA   Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to peptidase family A1.
DR   EMBL; AK082317; BAC38462.1; -.
DR   HSSP; P56817; 1FKN.
DR   MGD; MGI:1346542; Bace1.
DR   GO; GO:0005768; C:endosome; ISS.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   GO; GO:0005794; C:Golgi apparatus; ISS.
DR   GO; GO:0016021; C:integral to membrane; ISS.
DR   GO; GO:0004190; F:aspartic-type endopeptidase activity; ISS.
DR   GO; GO:0050435; P:beta-amyloid metabolism; ISS.
DR   GO; GO:0006509; P:membrane protein ectodomain proteolysis; ISS.
DR   InterPro; IPR001461; Peptidase_A1.
DR   InterPro; IPR009119; Pept_A1_BACE.
DR   InterPro; IPR009120; Pept_A1_BACE1.
DR   InterPro; IPR009007; Pept_Aspartic.
DR   InterPro; IPR001969; Pept_Asp_AS.
DR   PRINTS; PR01816; BACE1.
DR   PRINTS; PR01815; BACEFAMILY.
DR   PRINTS; PR00792; PEPSIN.
DR   PROSITE; PS00141; ASP_PROTEASE; 1.
KW   Aspartyl protease; Hydrolase; Protease.
SQ   SEQUENCE   467 AA;  52063 MW;  31AB674FF1843652 CRC64;

  Query Match             62.5%;  Score 10;  DB 2;  Length 467;
  Best Local Similarity   100.0%;  Pred. No. 0.05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 GIRLPLRSGL 13
              ||||||||||
Db         25 GIRLPLRSGL 34


RESULT 5
BAE1_MOUSE
ID   BAE1_MOUSE      STANDARD;      PRT;   501 AA.
AC   P56818;
DT   30-MAY-2000 (Rel. 39, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Beta-secretase 1 precursor (EC 3.4.23.46) (Beta-site APP cleaving
DE   enzyme 1) (Beta-site amyloid precursor protein cleaving enzyme 1)
DE   (Aspartyl protease 2) (Asp 2) (ASP2) (Membrane-associated aspartic
DE   protease 2) (Memapsin-2).
GN   Name=Bace1; Synonyms=Bace;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20002972; PubMed=10531052; DOI=10.1126/science.286.5440.735;
RA   Vassar R., Bennett B.D., Babu-Khan S., Kahn S., Mendiaz E.A.,
RA   Denis P., Teplow D.B., Ross S., Amarante P., Loeloff R., Luo Y.,
RA   Fisher S., Fuller J., Edenson S., Lile J., Jarosinski M.A.,
RA   Biere A.L., Curran E., Burgess T., Louis J.-C., Collins F.,
RA   Treanor J., Rogers G., Citron M.;
RT   "Beta-secretase cleavage of Alzheimer's amyloid precursor protein by
RT   the transmembrane aspartic protease BACE.";
RL   Science 286:735-741(1999).
RN   [2]
RP   REVISIONS TO 6 AND 81-87.
RA   Bennett B.D., Vassar R., Citron M.;
RL   Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20057170; PubMed=10591213; DOI=10.1038/990107;
RA   Yan R., Bienkowski M.J., Shuck M.E., Miao H., Tory M.C., Pauley A.M.,
RA   Brashier J.R., Stratman N.C., Mathews W.R., Buhl A.E., Carter D.B.,
RA   Tomasselli A.G., Parodi L.A., Heinrikson R.L., Gurney M.E.;
RT   "Membrane-anchored aspartyl protease with Alzheimer's disease beta-
RT   secretase activity.";
RL   Nature 402:533-537(1999).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Head;
RX   MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA   Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA   Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA   Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA   Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA   Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA   Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA   Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA   Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA   Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA   Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA   Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA   Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA   Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA   Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
```

```
RA   Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA   Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA   Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA   Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA   Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA   Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA   Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA   Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA   Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA   Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA   Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA   Birney E., Hayashizaki Y.;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6; TISSUE=Brain;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- FUNCTION: Responsible for the proteolytic processing of the
CC       amyloid precursor protein (APP). Cleaves at the amino terminus of
CC       the A-beta peptide sequence, between residues 671 and 672 of APP,
CC       leads to the generation and extracellular release of beta-cleaved
CC       soluble APP, and a corresponding cell-associated carboxy-terminal
CC       fragment which is later released by gamma-secretase (By
CC       similarity).
CC   -!- CATALYTIC ACTIVITY: Broad endopeptidase specificity. Cleaves Glu-
CC       Val-Asn-Leu-|-Asp-Ala-Glu-Phe in the Swedish variant of
CC       Alzheimer's amyloid precursor protein.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- TISSUE SPECIFICITY: Brain.
CC   -!- SIMILARITY: Belongs to the peptidase A1 family.
CC   ---------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; AF190726; AAF04143.2; -.
DR   EMBL; AF200346; AAF17082.1; -.
DR   EMBL; AK014464; BAB29370.1; -.
DR   EMBL; BC048189; AAH48189.1; -.
DR   HSSP; P56817; 1M4H.
DR   MEROPS; A01.004; -.
DR   MGD; MGI:1346542; Bace1.
DR   InterPro; IPR009119; Pept_A1_BACE.
DR   InterPro; IPR009120; Pept_A1_BACE1.
DR   InterPro; IPR001969; Pept_Asp_AS.
DR   InterPro; IPR009007; Pept_Aspartic.
DR   InterPro; IPR001461; Peptidase_A1.
DR   Pfam; PF00026; Asp; 1.
DR   PRINTS; PR01816; BACE1.
DR   PRINTS; PR01815; BACEFAMILY.
DR   PRINTS; PR00792; PEPSIN.
DR   PROSITE; PS00141; ASP_PROTEASE; 1.
KW   Aspartyl protease; Glycoprotein; Hydrolase; Signal; Transmembrane;
KW   Zymogen.
FT   SIGNAL       1    21       Potential.
FT   PROPEP      22    45       Potential.
FT   CHAIN       46   501       Beta-secretase 1.
FT   DOMAIN      22   457       Extracellular (Potential).
FT   TRANSMEM   458   478       Potential.
FT   DOMAIN     479   501       Cytoplasmic (Potential).
FT   ACT_SITE    93    93       By similarity.
FT   ACT_SITE   289   289       By similarity.
FT   DISULFID   216   420       By similarity.
FT   DISULFID   278   443       By similarity.
FT   DISULFID   330   380       By similarity.
FT   CARBOHYD   153   153       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   172   172       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   223   223       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   354   354       N-linked (GlcNAc. . .) (Potential).
SQ   SEQUENCE   501 AA;  55747 MW;  C085A013145E474E CRC64;

  Query Match             62.5%;  Score 10;  DB 1;  Length 501;
  Best Local Similarity   100.0%;  Pred. No. 0.053;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 GIRLPLRSGL 13
              ||||||||||
Db         25 GIRLPLRSGL 34


RESULT 6
BAE1_RAT
ID   BAE1_RAT       STANDARD;      PRT;   501 AA.
AC   P56819;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Beta-secretase 1 precursor (EC 3.4.23.46) (Beta-site APP cleaving
DE   enzyme 1) (Beta-site amyloid precursor protein cleaving enzyme 1)
DE   (Aspartyl protease 2) (Asp 2) (ASP2) (Membrane-associated aspartic
DE   protease 2) (Memapsin-2).
GN   Name=Bace1; Synonyms=Bace;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20002972; PubMed=10531052; DOI=10.1126/science.286.5440.735;
RA   Vassar R., Bennett B.D., Babu-Khan S., Kahn S., Mendiaz E.A.,
RA   Denis P., Teplow D.B., Ross S., Amarante P., Loeloff R., Luo Y.,
RA   Fisher S., Fuller J., Edenson S., Lile J., Jarosinski M.A.,
RA   Biere A.L., Curran E., Burgess T., Louis J.-C., Collins F.,
RA   Treanor J., Rogers G., Citron M.;
RT   "Beta-secretase cleavage of Alzheimer's amyloid precursor protein by
RT   the transmembrane aspartic protease BACE.";
RL   Science 286:735-741(1999).
CC   -!- FUNCTION: Responsible for the proteolytic processing of the
CC       amyloid precursor protein (APP). Cleaves at the amino terminus of
CC       the A-beta peptide sequence, between residues 671 and 672 of APP,
CC       leads to the generation and extracellular release of beta-cleaved
CC       soluble APP, and a corresponding cell-associated carboxy-terminal
CC       fragment which is later released by gamma-secretase (By
CC       similarity).
CC   -!- CATALYTIC ACTIVITY: Broad endopeptidase specificity. Cleaves Glu-
CC       Val-Asn-Leu-|-Asp-Ala-Glu-Phe in the Swedish variant of
CC       Alzheimer's amyloid precursor protein.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: Belongs to the peptidase A1 family.
CC   ---------------------------------------------------------------------------
```

```
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; AF190727; AAF04144.1; -.
DR   HSSP; P56817; 1M4H.
DR   MEROPS; A01.004; -.
DR   RGD; 2191; Bace.
DR   InterPro; IPR009119; Pept_A1_BACE.
DR   InterPro; IPR009120; Pept_A1_BACE1.
DR   InterPro; IPR001969; Pept_Asp_AS.
DR   InterPro; IPR009007; Pept_Aspartic.
DR   InterPro; IPR001461; Peptidase_A1.
DR   Pfam; PF00026; Asp; 1.
DR   PRINTS; PR01816; BACE1.
DR   PRINTS; PR01815; BACEFAMILY.
DR   PRINTS; PR00792; PEPSIN.
DR   PROSITE; PS00141; ASP_PROTEASE; 1.
KW   Aspartyl protease; Glycoprotein; Hydrolase; Signal; Transmembrane;
KW   Zymogen.
FT   SIGNAL        1     21       Potential.
FT   PROPEP       22     45       Potential.
FT   CHAIN        46    501       Beta-secretase 1.
FT   DOMAIN       22    457       Extracellular (Potential).
FT   TRANSMEM    458    478       Potential.
FT   DOMAIN      479    501       Cytoplasmic (Potential).
FT   ACT_SITE     93     93       By similarity.
FT   ACT_SITE    289    289       By similarity.
FT   DISULFID    216    420       By similarity.
FT   DISULFID    278    443       By similarity.
FT   DISULFID    330    380       By similarity.
FT   CARBOHYD    153    153       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    172    172       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    223    223       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    354    354       N-linked (GlcNAc. . .) (Potential).
SQ   SEQUENCE   501 AA;  55806 MW;  24B445BC8BE87DE3 CRC64;

  Query Match             62.5%;  Score 10;  DB 1;  Length 501;
  Best Local Similarity   100.0%;  Pred. No. 0.053;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 GIRLPLRSGL 13
              ||||||||||
Db         25 GIRLPLRSGL 34


RESULT 7
Q8BQY4
ID   Q8BQY4       PRELIMINARY;      PRT;   501 AA.
AC   Q8BQY4;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Mus musculus adult male corpora quadrigemina cDNA, RIKEN full-length
DE   enriched library, clone:B230346M13 product:beta-site APP cleaving
DE   enzyme, full insert sequence.
GN   Name=Bace1; Synonyms=Bace;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Meth. Enzymol. 303:19-44(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   RIKEN FANTOM Consortium;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [6]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
RA   Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA   Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA   Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA   Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA   Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA   Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA   Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA   Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA   Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA   Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA   Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to peptidase family A1.
DR   EMBL; AK046175; BAC32620.1; -.
DR   HSSP; P56817; 1FKN.
DR   MGD; MGI:1346542; Bace1.
DR   GO; GO:0005768; C:endosome; ISS.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   GO; GO:0005794; C:Golgi apparatus; ISS.
DR   GO; GO:0016021; C:integral to membrane; ISS.
DR   GO; GO:0004190; F:aspartic-type endopeptidase activity; ISS.
DR   GO; GO:0050435; P:beta-amyloid metabolism; ISS.
DR   GO; GO:0006509; P:membrane protein ectodomain proteolysis; ISS.
DR   InterPro; IPR001461; Peptidase_A1.
DR   InterPro; IPR009119; Pept_A1_BACE.
DR   InterPro; IPR009120; Pept_A1_BACE1.
DR   InterPro; IPR009007; Pept_Aspartic.
DR   InterPro; IPR001969; Pept_Asp_AS.
DR   PRINTS; PR01816; BACE1.
DR   PRINTS; PR01815; BACEFAMILY.
DR   PRINTS; PR00792; PEPSIN.
DR   PROSITE; PS00141; ASP_PROTEASE; 1.
KW   Aspartyl protease; Hydrolase; Protease.
```

```
SQ   SEQUENCE   501 AA;  55816 MW;  C0855513145E024E CRC64;

  Query Match             62.5%;  Score 10;  DB 2;  Length 501;
  Best Local Similarity   100.0%;  Pred. No. 0.053;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 GIRLPLRSGL 13
              ||||||||||
Db         25 GIRLPLRSGL 34


RESULT 8
Q8C7R1
ID   Q8C7R1      PRELIMINARY;      PRT;   501 AA.
AC   Q8C7R1;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Mus musculus 12 days embryo spinal cord cDNA, RIKEN full-length
DE   enriched library, clone:C530008K17 product:beta-site APP cleaving
DE   enzyme, full insert sequence.
GN   Name=Bace1; Synonyms=Bace;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Spinal cord;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Meth. Enzymol. 303:19-44(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Spinal cord;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   RIKEN FANTOM Consortium;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Spinal cord;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Spinal cord;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Spinal cord;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [6]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Spinal cord;
RA   Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA   Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA   Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA   Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA   Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA   Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA   Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA   Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA   Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA   Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA   Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to peptidase family A1.
DR   EMBL; AK049626; BAC33844.1; -.
DR   HSSP; P56817; 1FKN.
DR   MGD; MGI:1346542; Bace1.
DR   GO; GO:0005768; C:endosome; ISS.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   GO; GO:0005794; C:Golgi apparatus; ISS.
DR   GO; GO:0016021; C:integral to membrane; ISS.
DR   GO; GO:0004190; F:aspartic-type endopeptidase activity; ISS.
DR   GO; GO:0050435; P:beta-amyloid metabolism; ISS.
DR   GO; GO:0006509; P:membrane protein ectodomain proteolysis; ISS.
DR   InterPro; IPR001461; Peptidase_A1.
DR   InterPro; IPR009119; Pept_A1_BACE.
DR   InterPro; IPR009120; Pept_A1_BACE1.
DR   InterPro; IPR009007; Pept_Aspartic.
DR   InterPro; IPR001969; Pept_Asp_AS.
DR   PRINTS; PR01816; BACE1.
DR   PRINTS; PR01815; BACEFAMILY.
DR   PRINTS; PR00792; PEPSIN.
DR   PROSITE; PS00141; ASP_PROTEASE; 1.
KW   Aspartyl protease; Hydrolase; Protease.
SQ   SEQUENCE   501 AA;  55761 MW;  B410DA8B64647663 CRC64;

  Query Match             62.5%;  Score 10;  DB 2;  Length 501;
  Best Local Similarity   100.0%;  Pred. No. 0.053;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 GIRLPLRSGL 13
              ||||||||||
Db         25 GIRLPLRSGL 34


RESULT 9
Q7SZI8
ID   Q7SZI8      PRELIMINARY;      PRT;   814 AA.
AC   Q7SZI8;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   SMC1 alpha (Fragment).
OS   Oryzias latipes (Medaka fish) (Japanese ricefish).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC   Beloniformes; Adrianichthyidae; Oryziinae; Oryzias.
OX   NCBI_TaxID=8090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Testis;
RX   MEDLINE=22660315; PubMed=12759374;
RA   Lee J., Iwai T., Yokota T., Yamashita M.;
RT   "Temporally and spatially selective loss of Rec8 protein from meiotic
RT   chromosomes during mammalian meiosis.";
RL   J. Cell Sci. 116:2781-2790(2003).
CC   -!- SIMILARITY: Belongs to the ABC transporter family.
DR   EMBL; AB097255; BAC76893.1; -.
DR   HSSP; Q9X0R4; 1E69.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
```

```
DR   GO; GO:0007059; P:chromosome segregation; IEA.
DR   GO; GO:0006810; P:transport; IEA.
DR   InterPro; IPR003439; ABC_transporter.
DR   InterPro; IPR003405; SMC_C.
DR   InterPro; IPR010935; SMC_hinge.
DR   Pfam; PF02483; SMC_C; 1.
DR   Pfam; PF06470; SMC_hinge; 1.
DR   ProDom; PD000006; ABC_transporter; 1.
DR   PROSITE; PS00211; ABC_TRANSPORTER_1; UNKNOWN_1.
KW   ATP-binding.
FT   NON_TER       1      1
SQ   SEQUENCE   814 AA;  94132 MW;  8653E6C762EC6A5A CRC64;

  Query Match             50.0%;  Score 8;  DB 2;  Length 814;
  Best Local Similarity   100.0%;  Pred. No. 8.7;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 IRLPLRSG 12
              ||||||||
Db        521 IRLPLRSG 528


RESULT 10
Q9JPF6
ID   Q9JPF6      PRELIMINARY;      PRT;    97 AA.
AC   Q9JPF6;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein rth9.
GN   Name=rth9;
OS   Neisseria meningitidis.
OC   Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC   Neisseriaceae; Neisseria.
OX   NCBI_TaxID=487;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Z2491;
RX   MEDLINE=20187481; PubMed=10722605;
RX   DOI=10.1128/IAI.68.4.2082-2095.2000;
RA   Klee S.R., Nassif X., Kusecek B., Merker P., Beretti J.L., Achtman M.,
RA   Tinsley C.R.;
RT   "Molecular and biological analysis of eight genetic islands that
RT   distinguish Neisseria meningitidis from the closely related pathogen
RT   Neisseria gonorrhoeae.";
RL   Infect. Immun. 68:2082-2095(2000).
DR   EMBL; AJ391256; CAB71967.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   97 AA;  10716 MW;  7EDF863F7B6531F9 CRC64;

  Query Match             43.8%;  Score 7;  DB 2;  Length 97;
  Best Local Similarity   100.0%;  Pred. No. 15;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 LRSGLGG 15
              |||||||
Db         81 LRSGLGG 87


RESULT 11
Q9JTC5
ID   Q9JTC5      PRELIMINARY;      PRT;   125 AA.
AC   Q9JTC5;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Hypothetical protein NMA1874.
GN   OrderedLocusNames=NMA1874;
OS   Neisseria meningitidis (serogroup A).
OC   Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC   Neisseriaceae; Neisseria.
OX   NCBI_TaxID=65699;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Z2491 / Serogroup A / Serotype 4A;
RX   MEDLINE=20222556; PubMed=10761919; DOI=10.1038/35006655;
RA   Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.M.,
RA   Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
RA   Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
RA   Jagels K., Leather S., Moule S., Mungall K.L., Quail M.A.,
RA   Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
RA   Whitehead S., Spratt B.G., Barrell B.G.;
RT   "Complete DNA sequence of a serogroup A strain of Neisseria
RT   meningitidis Z2491.";
RL   Nature 404:502-506(2000).
DR   EMBL; AL162757; CAB85097.1; -.
DR   PIR; E81814; E81814.
KW   Complete proteome; Hypothetical protein.
SQ   SEQUENCE   125 AA;  13950 MW;  5B9C7D782E89884D CRC64;

  Query Match             43.8%;  Score 7;  DB 2;  Length 125;
  Best Local Similarity   100.0%;  Pred. No. 19;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 LRSGLGG 15
              |||||||
Db        109 LRSGLGG 115


RESULT 12
Q7NTK4
ID   Q7NTK4      PRELIMINARY;      PRT;   181 AA.
AC   Q7NTK4;
DT   01-MAR-2004 (TrEMBLrel. 26, Created)
DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Cytochrome b561.
GN   Name=cybB; OrderedLocusNames=CV3050;
OS   Chromobacterium violaceum.
OC   Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC   Neisseriaceae; Chromobacterium.
OX   NCBI_TaxID=536;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ATCC 12472 / DSM 30191;
RX   MEDLINE=22882880; PubMed=14500782; DOI=10.1073/pnas.1832124100;
RA   Vasconcelos A.T.R., de Almeida D.F., Hungria M., Guimaraes C.T.,
RA   Antonio R.V., Almeida F.C., de Almeida L.G.P., de Almeida R.,
RA   Alves-Gomes J.A., Andrade E.M., Araripe J., de Araujo M.F.F.,
RA   Astolfi-Filho S., Azevedo V., Baptista A.J., Bataus L.A.M.,
RA   Batista J.S., Belo A., van den Berg C., Bogo M., Bonatto S.,
RA   Bordignon J., Brigido M.M., Brito C.A., Brocchi M., Burity H.A.,
RA   Camargo A.A., Cardoso D.D.P., Carneiro N.P., Carraro D.M.,
RA   Carvalho C.M.B., Cascardo J.C.M., Cavada B.S., Chueire L.M.O.,
RA   Creczynski-Pasa T.B., Cunha-Junior N.C., Fagundes N., Falcao C.L.,
RA   Fantinatti F., Farias I.P., Felipe M.S.S., Ferrari L.P., Ferro J.A.,
RA   Ferro M.I.T., Franco G.R., Freitas N.S.A., Furlan L.R.,
RA   Gazzinelli R.T., Gomes E.A., Goncalves P.R., Grangeiro T.B.,
RA   Grattapaglia D., Grisard E.C., Hanna E.S., Jardim S.N., Laurino J.,
RA   Leoi L.C.T., Lima L.F.A., Loureiro M.F., Lyra M.C.C.P.,
RA   Madeira H.M.F., Manfio G.P., Maranhao A.Q., Martins W.S.,
RA   di Mauro S.M.Z., de Medeiros S.R.B., Meissner R.V., Moreira M.A.M.,
RA   Nascimento F.F., Nicolas M.F., Oliveira J.G., Oliveira S.C.,
RA   Paixao R.F.C., Parente J.A., Pedrosa F.O., Pena S.D.J., Pereira J.O.,
RA   Pereira M., Pinto L.S.R.C., Pinto L.S., Porto J.I.R., Potrich D.P.,
RA   Ramalho-Neto C.E., Reis A.M.M., Rigo L.U., Rondinelli E.,
RA   Santos E.B.P., Santos F.R., Schneider M.P.C., Seuanez H.N.,
RA   Silva A.M.R., da Silva A.L.C., Silva D.W., Silva R., Simoes I.C.,
RA   Simon D., Soares C.M.A., Soares R.B.A., Souza E.M., Souza K.R.L.,
RA   Souza R.C., Steffens M.B.R., Steindel M., Teixeira S.R., Urmenyi T.,
RA   Vettore A., Wassem R., Zaha A., Simpson A.J.G.;
RT   "The complete genome sequence of Chromobacterium violaceum reveals
RT   remarkable and exploitable bacterial adaptability.";
RL   Proc. Natl. Acad. Sci. U.S.A. 100:11660-11665(2003).
DR   EMBL; AE016920; AAQ60719.1; -.
DR   InterPro; IPR011577; CytB561_bact.
```

```
DR   Pfam; PF01292; Ni_hydr_CYTB; 1.
KW   Complete proteome.
SQ   SEQUENCE   181 AA;  19650 MW;  94FBFFB853494F08 CRC64;

  Query Match             43.8%;  Score 7;  DB 2;  Length 181;
  Best Local Similarity   100.0%;  Pred. No. 26;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 PLRSGLG 14
              |||||||
Db         42 PLRSGLG 48


RESULT 13
Q66F29
ID   Q66F29      PRELIMINARY;      PRT;   239 AA.
AC   Q66F29;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Putative ABC phosphonate transporter, ATP binding protein, also
DE   putative C-P lyase component.
GN   Name=phnL; ORFNames=YPTB0511;
OS   Yersinia pseudotuberculosis IP 32953.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Yersinia.
OX   NCBI_TaxID=273123;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=IP 32953;
RX   PubMed=15358858;
RA   Chain P.S.G., Carniel E., Larimer F.W., Lamerdin J., Stoutland P.O.,
RA   Regala W.M., Georgescu A.M., Vergez L.M., Land M.L., Motin L.V.,
RA   Brubaker R.R., Fowler J., Hinnebusch B.J., Marceau M., Medigue C.,
RA   Simonet M., Chenal-Francisque V., Souza B., Dacheux D., Elliott J.M.,
RA   Derbise A., Hauser L.J., Garcia E.;
RT   "Insights into the genome evolution of Yersinia pestis through whole
RT   genome comparison with Yersinia pseudotuberculosis.";
RL   Proc. Natl. Acad. Sci. U.S.A. 101:13826-13831(2004).
DR   EMBL; BX936398; CAH19751.1; -.
DR   GO; GO:0016829; F:lyase activity; IEA.
DR   InterPro; IPR003593; AAA_ATPase.
DR   InterPro; IPR003439; ABC_transporter.
DR   Pfam; PF00005; ABC_tran; 1.
DR   ProDom; PD000006; ABC_transporter; 1.
DR   SMART; SM00382; AAA; 1.
DR   PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR   PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
KW   ATP-binding; Lyase.
SQ   SEQUENCE   239 AA;  26695 MW;  4096220E6760B9FB CRC64;

  Query Match             43.8%;  Score 7;  DB 2;  Length 239;
  Best Local Similarity   100.0%;  Pred. No. 32;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 QHGIRLP 8
              |||||||
Db         20 QHGIRLP 26


RESULT 14
Q8ZBF4
ID   Q8ZBF4      PRELIMINARY;      PRT;   239 AA.
AC   Q8ZBF4; Q7CKG6;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Phosphonates transport ATP-binding protein (ATP-binding component of
DE   phosphonate ABC transporter).
GN   Name=phnL; OrderedLocusNames=YPO3462, y0723;
OS   Yersinia pestis.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Yersinia.
OX   NCBI_TaxID=632;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CO-92 / Biovar Orientalis;
RX   MEDLINE=21470413; PubMed=11586360; DOI=10.1038/35097083;
RA   Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
RA   Prentice M.B., Sebaihia M., James K.D., Churcher C.M., Mungall K.L.,
RA   Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.-M.,
RA   Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA   Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
RA   Leather S., Moule S., Oyston P.C.F., Quail M.A., Rutherford K.M.,
RA   Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
RT   "Genome sequence of Yersinia pestis, the causative agent of plague.";
RL   Nature 413:523-527(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=KIM5 / Biovar Mediaevalis;
RX   MEDLINE=22137863; PubMed=12142430;
RX   DOI=10.1128/JB.184.16.4601-4611.2002;
RA   Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
RA   Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
RA   Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
RA   Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
RA   Perry R.D.;
RT   "Genome sequence of Yersinia pestis KIM.";
RL   J. Bacteriol. 184:4601-4611(2002).
CC   -!- SIMILARITY: Belongs to the ABC transporter family.
DR   EMBL; AJ414157; CAC92691.1; -.
DR   EMBL; AE013674; AAM84311.1; -.
DR   PIR; AG0420; AG0420.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
DR   GO; GO:0000166; F:nucleotide binding; IEA.
DR   GO; GO:0006810; P:transport; IEA.
DR   Pfam; PF00005; ABC_tran; 1.
DR   ProDom; PD000006; ABC_transporter; 1.
DR   SMART; SM00382; AAA; 1.
DR   PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR   PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
KW   ATP-binding; Complete proteome.
SQ   SEQUENCE   239 AA;  26667 MW;  59AB94CC3760B9FB CRC64;

  Query Match             43.8%;  Score 7;  DB 2;  Length 239;
  Best Local Similarity   100.0%;  Pred. No. 32;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 QHGIRLP 8
              |||||||
Db         20 QHGIRLP 26


RESULT 15
Q9RXU2
ID   Q9RXU2      PRELIMINARY;      PRT;   259 AA.
AC   Q9RXU2;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Hypothetical protein DR0214.
GN   OrderedLocusNames=DR0214;
OS   Deinococcus radiodurans.
OC   Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales;
OC   Deinococcaceae; Deinococcus.
OX   NCBI_TaxID=1299;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=R1 / ATCC 13939 / DSM 20539 / NCIB 9279;
RX   MEDLINE=20036896; PubMed=10567266; DOI=10.1126/science.286.5444.1571;
RA   White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
RA   Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA   Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
RA   Vamathevan J.J., Lam P., McDonald L.A., Utterback T.R., Zalewski C.,
```

RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
RA Ketchum K.A., Nelson K.E., Salzberg S.L., Smith H.O., Venter J.C.,
RA Fraser C.M.;
RT "Genome sequence of the radioresistant bacterium Deinococcus
RT radiodurans R1.";
RL Science 286:1571-1577(1999).
DR EMBL; AE001883; AAF09805.1; -.
DR PIR; A75547; A75547.
DR TIGR; DR0214; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 259 AA; 29103 MW; 49522C0ADD9327CF CRC64;

Query Match 43.8%; Score 7; DB 2; Length 259;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 HGIRLPL 9
|||||||
Db 190 HGIRLPL 196

Search completed: July 26, 2005, 16:37:18
Job time : 175 secs

GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: July 27, 2005, 18:18:13 ; Search time 1937 Seconds
(without alignments)
400.250 Million cell updates/sec

Title: US-10-726-967A-3
Perfect score: 16
Sequence: 1 TQHGIRLPLRSGLGGA 16

Scoring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Word size: 1

Total number of hits satisfying chosen parameters: 9404934

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US10726967/runat_26072005_130815_6474/app_query.fasta_1.199
-DB=GenEmbl -QFMT=fastap -SUFFIX=olip2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10726967_@CGN_1_1_5600_@runat_26072005_130815_6474 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	16	100.0	517	9	AB089958	AB089958 Homo sapi
2	16	100.0	1287	6	AR224122	AR224122 Sequence
3	16	100.0	1287	6	AR269253	AR269253 Sequence
4	16	100.0	1287	6	AR478808	AR478808 Sequence
5	16	100.0	1287	6	AR487374	AR487374 Sequence
6	16	100.0	1287	6	AR532014	AR532014 Sequence
7	16	100.0	1287	6	AR540915	AR540915 Sequence
8	16	100.0	1287	6	AR560125	AR560125 Sequence
9	16	100.0	1287	6	AX105432	AX105432 Sequence
10	16	100.0	1287	6	AX573870	AX573870 Sequence
11	16	100.0	1302	6	BD235897	BD235897 Alzheimer
12	16	100.0	1302	6	AR224103	AR224103 Sequence
13	16	100.0	1302	6	AR269234	AR269234 Sequence
14	16	100.0	1302	6	AR478789	AR478789 Sequence
15	16	100.0	1302	6	AR487355	AR487355 Sequence
16	16	100.0	1302	6	AR531995	AR531995 Sequence
17	16	100.0	1302	6	AR540896	AR540896 Sequence
18	16	100.0	1302	6	AR560106	AR560106 Sequence
19	16	100.0	1302	6	AX105407	AX105407 Sequence
20	16	100.0	1302	6	AX573845	AX573845 Sequence
21	16	100.0	1302	6	AX700454	AX700454 Sequence
22	16	100.0	1305	6	AR224123	AR224123 Sequence
23	16	100.0	1305	6	AR269254	AR269254 Sequence
24	16	100.0	1305	6	AR478809	AR478809 Sequence
25	16	100.0	1305	6	AR487375	AR487375 Sequence
26	16	100.0	1305	6	AR532015	AR532015 Sequence
27	16	100.0	1305	6	AR540916	AR540916 Sequence
28	16	100.0	1305	6	AR560126	AR560126 Sequence
29	16	100.0	1305	6	AX105434	AX105434 Sequence
30	16	100.0	1305	6	AX573872	AX573872 Sequence
31	16	100.0	1333	9	AB050438	AB050438 Homo sapi
32	16	100.0	1341	6	BD235895	BD235895 Alzheimer
33	16	100.0	1341	6	AR224101	AR224101 Sequence
34	16	100.0	1341	6	AR269232	AR269232 Sequence
35	16	100.0	1341	6	AR478787	AR478787 Sequence
36	16	100.0	1341	6	AR487353	AR487353 Sequence
37	16	100.0	1341	6	AR531993	AR531993 Sequence
38	16	100.0	1341	6	AR540894	AR540894 Sequence
39	16	100.0	1341	6	AR560104	AR560104 Sequence
40	16	100.0	1341	6	AX105403	AX105403 Sequence
41	16	100.0	1341	6	AX573841	AX573841 Sequence
42	16	100.0	1362	6	BD235899	BD235899 Alzheimer
43	16	100.0	1362	6	AR224105	AR224105 Sequence
44	16	100.0	1362	6	AR269236	AR269236 Sequence
45	16	100.0	1362	6	AR478791	AR478791 Sequence

ALIGNMENTS

RESULT 1
AB089958
LOCUS AB089958 517 bp mRNA linear PRI 19-AUG-2003
DEFINITION Homo sapiens BACE mRNA for beta-site APP cleaving enzyme isoform I-127, complete cds.
ACCESSION AB089958
VERSION AB089958.1 GI:34014375
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Tanahashi,H.
TITLE A novel alternatively spliced isoform of BACE, I-127 induced by cycloheximide treatment
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 517)
AUTHORS Tanahashi,H.
TITLE Direct Submission
JOURNAL Submitted (17-AUG-2002) Hiroshi Tanahashi, National Institute of Neuroscience, Division of Demyelinating Disease and Aging; 4-1-1 Ogawahigashi, Kodaira, Tokyo 187-8502, Japan
(E-mail:tanahash@ncnp.go.jp, Tel:81-042-341-2711(ex.5163), Fax:81-042-346-1747)
FEATURES Location/Qualifiers
source 1. .517
/organism="Homo sapiens"

```
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /chromosome="11"
                     /map="11q23.2-23.3"
                     /cell_line="human neuroblastoma SH-SY5Y"
     gene            /note="I-127 is induced by cycloheximide treatment.
                     Alternative splicing of the RNA occurs at an internal
     CDS             donor in exon 3."
                     1. .517
                     /gene="BACE"
                     1. .384
                     /gene="BACE"
                     /codon_start=1
                     /product="beta-site APP cleaving enzyme isoform I-127"
                     /protein_id="BAC81826.1"
                     /db_xref="GI:34014376"
ORIGIN               /translation="MAQALPWLLLWMGAGVLPAHGTQHGIRLPLRSGLGGAPLGLRLP
                     RETDEEPEEPGRRGSFVEMVDNLRGKSGQGYYVEMTVGSPPQTLNILVDTGSSNFAVG
                     AAPHPFLHRYYQRQLSSTYRDLRKA"

Alignment Scores:
Pred. No.:
Score:                          1.59e-06
Percent Similarity:             16.00           Length:
Best Local Similarity:          100.00%         Matches:        517
Query Match:                    100.00%         Conservative:   16
DB:                             9               Mismatches:     0
                                                Indels:         0
US-10-726-967A-3 (1-16) x AB089958 (1-517)      Gaps:           0

Qy          1 ThrGlnHisGlyIleArgLeuProLeuArgSerGlyLeuGlyGlyAla 16
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 ACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCC 111

RESULT 2
AR224122
LOCUS
DEFINITION  AR224122
ACCESSION   Sequence 50 from patent US 6440698.                1287 bp    DNA     linear   PAT 26-SEP-2002
VERSION     AR224122
KEYWORDS    AR224122.1  GI:23332782
SOURCE      .
  ORGANISM  Unknown.
            Unknown.
REFERENCE   Unclassified.
  AUTHORS   1  (bases 1 to 1287)
            Gurney,M.E., Bienkowski,M.J., Heinrikson,R.L., Parodi,L.A. and
            Yan,R.
  TITLE     Alzheimer's disease secretase, APP substrates therefor, and uses
            therefor
  JOURNAL   Patent: US 6440698-A 50 27-AUG-2002;
FEATURES
     source          Location/Qualifiers
                     1. .1287
                     /organism="unknown"
ORIGIN               /mol_type="genomic DNA"

Alignment Scores:
Pred. No.:
Score:                          3.27e-06
Percent Similarity:             16.00           Length:
Best Local Similarity:          100.00%         Matches:        1287
Query Match:                    100.00%         Conservative:   16
DB:                             6               Mismatches:     0
                                                Indels:         0
US-10-726-967A-3 (1-16) x AR224122 (1-1287)     Gaps:           0

Qy          1 ThrGlnHisGlyIleArgLeuProLeuArgSerGlyLeuGlyGlyAla 16
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 ACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCC 111

RESULT 3
AR269253
LOCUS
DEFINITION  AR269253
ACCESSION   Sequence 50 from patent US 6500667.                1287 bp    DNA     linear   PAT 10-APR-2003
VERSION     AR269253.1  GI:29700221
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1287)
  AUTHORS   Gurney,M.E., Bienkowski,M.J., Heinrikson,R.L., Parodi,L.A. and
            Yan,R.
  TITLE     Aspartyl protease 2 (Asp2) antisense oligonucleotides
  JOURNAL   Patent: US 6500667-A 50 31-DEC-2002;
FEATURES
     source          Location/Qualifiers
                     1. .1287
                     /organism="unknown"
ORIGIN               /mol_type="genomic DNA"

Alignment Scores:
Pred. No.:
Score:                          3.27e-06
Percent Similarity:             16.00           Length:
Best Local Similarity:          100.00%         Matches:        1287
Query Match:                    100.00%         Conservative:   16
DB:                             6               Mismatches:     0
                                                Indels:         0
US-10-726-967A-3 (1-16) x AR269253 (1-1287)     Gaps:           0

Qy          1 ThrGlnHisGlyIleArgLeuProLeuArgSerGlyLeuGlyGlyAla 16
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 ACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCC 111

RESULT 4
AR478808
LOCUS
DEFINITION  AR478808
ACCESSION   Sequence 50 from patent US 6699671.                1287 bp    DNA     linear   PAT 14-MAY-2004
VERSION     AR478808
KEYWORDS    AR478808.1  GI:47237528
SOURCE      .
  ORGANISM  Unknown.
            Unknown.
REFERENCE   Unclassified.
  AUTHORS   1  (bases 1 to 1287)
            Gurney,M.E., Bienkowski,M.J., Heinrikson,R.L., Parodi,L.A. and
            Yan,R.
  TITLE     Alzheimer's disease secretase, APP substrates therefor, and uses
            therefor
  JOURNAL   Patent: US 6699671-A 50 02-MAR-2004;
FEATURES
     source          Location/Qualifiers
                     1. .1287
                     /organism="unknown"
ORIGIN               /mol_type="genomic DNA"

Alignment Scores:
Pred. No.:
Score:                          3.27e-06
Percent Similarity:             16.00           Length:
Best Local Similarity:          100.00%         Matches:        1287
Query Match:                    100.00%         Conservative:   16
DB:                             6               Mismatches:     0
                                                Indels:         0
US-10-726-967A-3 (1-16) x AR478808 (1-1287)     Gaps:           0

Qy          1 ThrGlnHisGlyIleArgLeuProLeuArgSerGlyLeuGlyGlyAla 16
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 ACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCC 111

RESULT 5
AR487374
LOCUS
DEFINITION  AR487374
            Sequence 50 from patent US 6706485                 1287 bp    DNA     linear   PAT 14-MAY-2004
```

```
ACCESSION   AR487374
VERSION     AR487374.1  GI:47252472
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1287)
  AUTHORS   Gurney,M.E., Bienkowski,M.J., Heinrikson,R.L., Parodi,L.A. and
            Yan,R.
  TITLE     Method of identifying agents that inhibit APP processing activity
  JOURNAL   Patent: US 6706485-A 50 16-MAR-2004;
FEATURES             Location/Qualifiers
     source          1. .1287
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:                3.27e-06       Length:          1287
Score:                    16.00          Matches:         16
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              100.00%        Indels:          0
DB:                       6              Gaps:            0

US-10-726-967A-3 (1-16) x AR487374 (1-1287)

Qy          1 ThrGlnHisGlyIleArgLeuProLeuArgSerGlyLeuGlyGlyAla 16
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 ACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCC 111

RESULT 6
AR532014
LOCUS       AR532014                1287 bp    DNA     linear   PAT 08-OCT-2004
DEFINITION  Sequence 50 from patent US 6727074.
ACCESSION   AR532014
VERSION     AR532014.1  GI:53920548
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1287)
  AUTHORS   Gurney,M.E., Bienkowski,M.J., Heinrikson,R.L., Parodi,L.A. and
            Yan,R.
  TITLE     Alzheimer's disease secretase, APP substrates therefor, and uses
            therefor
  JOURNAL   Patent: US 6727074-A 50 27-APR-2004;
FEATURES             Location/Qualifiers
     source          1. .1287
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:                3.27e-06       Length:          1287
Score:                    16.00          Matches:         16
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              100.00%        Indels:          0
DB:                       6              Gaps:            0

US-10-726-967A-3 (1-16) x AR532014 (1-1287)

Qy          1 ThrGlnHisGlyIleArgLeuProLeuArgSerGlyLeuGlyGlyAla 16
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 ACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCC 111

RESULT 7
AR540915
LOCUS       AR540915                1287 bp    DNA     linear   PAT 08-OCT-2004
DEFINITION  Sequence 50 from patent US 6737510.
ACCESSION   AR540915
VERSION     AR540915.1  GI:53932428
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1287)
  AUTHORS   Gurney,M.E., Bienkowski,M.J., Heinrikson,R.L., Parodi,L.A. and
            Yan,R.
  TITLE     Alzheimer's disease secretase, APP substrates therefor, and uses
            thereof
  JOURNAL   Patent: US 6737510-A 50 18-MAY-2004;
FEATURES             Location/Qualifiers
     source          1. .1287
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:                3.27e-06       Length:          1287
Score:                    16.00          Matches:         16
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              100.00%        Indels:          0
DB:                       6              Gaps:            0

US-10-726-967A-3 (1-16) x AR540915 (1-1287)

Qy          1 ThrGlnHisGlyIleArgLeuProLeuArgSerGlyLeuGlyGlyAla 16
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 ACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCC 111

RESULT 8
AR560125
LOCUS       AR560125                1287 bp    DNA     linear   PAT 08-OCT-2004
DEFINITION  Sequence 50 from patent US 6753163.
ACCESSION   AR560125
VERSION     AR560125.1  GI:53970492
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1287)
  AUTHORS   Gurney,M.E., Bienkowski,M.J., Heinrikson,R.L., Parodi,L.A. and
            Yan,R.
  TITLE     Alzheimer's disease secretase, APP substrates therefor, and uses
            therefor
  JOURNAL   Patent: US 6753163-A 50 22-JUN-2004;
FEATURES             Location/Qualifiers
     source          1. .1287
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:                3.27e-06       Length:          1287
Score:                    16.00          Matches:         16
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              100.00%        Indels:          0
DB:                       6              Gaps:            0

US-10-726-967A-3 (1-16) x AR560125 (1-1287)

Qy          1 ThrGlnHisGlyIleArgLeuProLeuArgSerGlyLeuGlyGlyAla 16
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 ACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCC 111

RESULT 9
AX105432
LOCUS       AX105432                1287 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 50 from Patent WO0123533.
ACCESSION   AX105432
VERSION     AX105432.1  GI:13921541
KEYWORDS    .
```

```
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Gurney,M. and Bienkowski,M.J.
  TITLE     Alzheimer's disease secretase, app substrates therefor, and uses
            therefor
  JOURNAL   Patent: WO 0123533-A 50 05-APR-2001;
            Pharmacia & Upjohn Company (US)
FEATURES             Location/Qualifiers
     source          1. .1287
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Hu-Asp2(b) delta TM"
ORIGIN

Alignment Scores:
Pred. No.:                3.27e-06        Length:          1287
Score:                    16.00           Matches:         16
Percent Similarity:       100.00%         Conservative:    0
Best Local Similarity:    100.00%         Mismatches:      0
Query Match:              100.00%         Indels:          0
DB:                       6               Gaps:            0

US-10-726-967A-3 (1-16) x AX105432 (1-1287)

Qy          1 ThrGlnHisGlyIleArgLeuProLeuArgSerGlyLeuGlyGlyAla 16
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 ACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCC 111

RESULT 10
AX573870
LOCUS       AX573870                1287 bp    DNA     linear   PAT 07-JAN-2003
DEFINITION  Sequence 50 from Patent EP1249498.
ACCESSION   AX573870
VERSION     AX573870.1  GI:27551507
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Gurney,M. and Bienkowski,M.J.
  TITLE     Alzheimer's disease secretase, app substrates therefor, and uses
            therefor
  JOURNAL   Patent: EP 1249498-A 50 16-OCT-2002;
            PHARMACIA & UPJOHN COMPANY (US)
FEATURES             Location/Qualifiers
     source          1. .1287
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Hu-Asp2(b) delta TM"
ORIGIN

Alignment Scores:
Pred. No.:                3.27e-06        Length:          1287
Score:                    16.00           Matches:         16
Percent Similarity:       100.00%         Conservative:    0
Best Local Similarity:    100.00%         Mismatches:      0
Query Match:              100.00%         Indels:          0
DB:                       6               Gaps:            0

US-10-726-967A-3 (1-16) x AX573870 (1-1287)

Qy          1 ThrGlnHisGlyIleArgLeuProLeuArgSerGlyLeuGlyGlyAla 16
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 ACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCC 111

RESULT 11
BD235897
LOCUS       BD235897                1302 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Alzheimer's disease secretase.
ACCESSION   BD235897
VERSION     BD235897.1  GI:33045667
KEYWORDS    JP 2002526081-A/13.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1302)
  AUTHORS   Gurney,M.E., Bienkowski,M.J., Heinrikson,R.L., Parodi,L.A. and
            Yan,R.
  TITLE     Alzheimer's disease secretase
  JOURNAL   Patent: JP 2002526081-A 13 20-AUG-2002;
            PHARMACIA AND UPJOHN CO
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002526081-A/13
            PD   20-AUG-2002
            PF   23-SEP-1999 JP 2000574268
            PR   24-SEP-1998 US    60/101594
            PI   MARK E GURNEY,MICHAEL JEROME BIENKOWSKI,ROBERT LEROY  PI
            HEINRIKSON,
            PI   LUIS A PARODI,RIQIANG YAN
            PC   C12N15/09,A61K45/00,A61P25/28,C07K14/47,C07K16/18,C12N1/15, PC
              C12N1/19,
            PC
            C12N1/21,C12N5/10,C12N9/64,C12P21/02,C12P21/08,C12Q1/37,G01N33/ PC
             15,
            PC   G01N33/50//(C12N1/21,C12R1:19),C12N15/00,C12N5/00 CC
            Alzheimer's disease secretase
            FH   Key             Location/Qualifiers
            FT   source          1. .1302
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .1302
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
ORIGIN

Alignment Scores:
Pred. No.:                3.3e-06         Length:          1302
Score:                    16.00           Matches:         16
Percent Similarity:       100.00%         Conservative:    0
Best Local Similarity:    100.00%         Mismatches:      0
Query Match:              100.00%         Indels:          0
DB:                       6               Gaps:            0

US-10-726-967A-3 (1-16) x BD235897 (1-1302)

Qy          1 ThrGlnHisGlyIleArgLeuProLeuArgSerGlyLeuGlyGlyAla 16
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db          4 ACTCAGCATGGTATTCGTCTGCCACTGCGTAGCGGTCTGGGTGGTGCT 51

RESULT 12
AR224103
LOCUS       AR224103                1302 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 25 from patent US 6440698.
ACCESSION   AR224103
VERSION     AR224103.1  GI:23332763
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1302)
  AUTHORS   Gurney,M.E., Bienkowski,M.J., Heinrikson,R.L., Parodi,L.A. and
            Yan,R.
  TITLE     Alzheimer's disease secretase, APP substrates therefor, and uses
            therefor
  JOURNAL   Patent: US 6440698-A 25 27-AUG-2002;
FEATURES             Location/Qualifiers
     source          1. .1302
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN
```

```
Alignment Scores:
Pred. No.:              3.3e-06         Length:         1302
Score:                  16.00           Matches:        16
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     6               Gaps:           0

US-10-726-967A-3 (1-16) x AR224103 (1-1302)

Qy          1 ThrGlnHisGlyIleArgLeuProLeuArgSerGlyLeuGlyGlyAla 16
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db          4 ACTCAGCATGGTATTCGTCTGCCACTGCGTAGCGGTCTGGGTGGTGCT 51

RESULT 13
AR269234
LOCUS       AR269234                1302 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 25 from patent US 6500667.
ACCESSION   AR269234
VERSION     AR269234.1  GI:29700202
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1302)
  AUTHORS   Gurney,M.E., Bienkowski,M.J., Heinrikson,R.L., Parodi,L.A. and
            Yan,R.
  TITLE     Aspartyl protease 2 (Asp2) antisense oligonucleotides
  JOURNAL   Patent: US 6500667-A 25 31-DEC-2002;
FEATURES             Location/Qualifiers
     source          1. .1302
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              3.3e-06         Length:         1302
Score:                  16.00           Matches:        16
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     6               Gaps:           0

US-10-726-967A-3 (1-16) x AR269234 (1-1302)

Qy          1 ThrGlnHisGlyIleArgLeuProLeuArgSerGlyLeuGlyGlyAla 16
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db          4 ACTCAGCATGGTATTCGTCTGCCACTGCGTAGCGGTCTGGGTGGTGCT 51

RESULT 14
AR478789
LOCUS       AR478789                1302 bp    DNA     linear   PAT 14-MAY-2004
DEFINITION  Sequence 25 from patent US 6699671.
ACCESSION   AR478789
VERSION     AR478789.1  GI:47237509
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1302)
  AUTHORS   Gurney,M.E., Bienkowski,M.J., Heinrikson,R.L., Parodi,L.A. and
            Yan,R.
  TITLE     Alzheimer's disease secretase, APP substrates therefor, and uses
            therefor
  JOURNAL   Patent: US 6699671-A 25 02-MAR-2004;
FEATURES             Location/Qualifiers
     source          1. .1302
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              3.3e-06         Length:         1302
Score:                  16.00           Matches:        16
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     6               Gaps:           0

US-10-726-967A-3 (1-16) x AR478789 (1-1302)

Qy          1 ThrGlnHisGlyIleArgLeuProLeuArgSerGlyLeuGlyGlyAla 16
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db          4 ACTCAGCATGGTATTCGTCTGCCACTGCGTAGCGGTCTGGGTGGTGCT 51

RESULT 15
AR487355
LOCUS       AR487355                1302 bp    DNA     linear   PAT 14-MAY-2004
DEFINITION  Sequence 25 from patent US 6706485.
ACCESSION   AR487355
VERSION     AR487355.1  GI:47252453
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1302)
  AUTHORS   Gurney,M.E., Bienkowski,M.J., Heinrikson,R.L., Parodi,L.A. and
            Yan,R.
  TITLE     Method of identifying agents that inhibit APP processing activity
  JOURNAL   Patent: US 6706485-A 25 16-MAR-2004;
FEATURES             Location/Qualifiers
     source          1. .1302
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              3.3e-06         Length:         1302
Score:                  16.00           Matches:        16
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     6               Gaps:           0

US-10-726-967A-3 (1-16) x AR487355 (1-1302)

Qy          1 ThrGlnHisGlyIleArgLeuProLeuArgSerGlyLeuGlyGlyAla 16
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db          4 ACTCAGCATGGTATTCGTCTGCCACTGCGTAGCGGTCTGGGTGGTGCT 51


Search completed: July 27, 2005, 19:43:12
Job time : 1938 secs
```

GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: July 27, 2005, 17:25:16 ; Search time 432 Seconds
(without alignments)
219.250 Million cell updates/sec

Title: US-10-726-967A-3
Perfect score: 16
Sequence: 1 TQHGIRLPLRSGLGGA 16

Scoring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Word size: 1

Total number of hits satisfying chosen parameters: 8770599

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US10726967/runat_26072005_130815_6465/app_query.fasta_1.199
-DB=N_Geneseq_16Dec04 -QFMT=fastap -SUFFIX=olip2n.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10726967_@CGN_1_1_708_@runat_26072005_130815_6465 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : N_Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	16	100.0	1287	4	AAD17895	Aad17895 Human-Asp
2	16	100.0	1287	4	AAD13276	Aad13276 Human-Asp
3	16	100.0	1287	4	AAD06768	Aad06768 Human asp
4	16	100.0	1287	4	AAS11547	Aas11547 Human cDN
5	16	100.0	1287	6	ABL52487	Abl52487 Human Asp
6	16	100.0	1287	12	ADJ94362	Adj94362 Human-pro
7	16	100.0	1287	12	ADO50458	Ado50458 Human Asp
8	16	100.0	1287	13	ADR75371	Adr75371 Human Asp
9	16	100.0	1302	3	AAA15670	Aaa15670 Human-pro
10	16	100.0	1302	4	AAS11713	Aas11713 DNA encod
11	16	100.0	1302	4	AAD17876	Aad17876 Human-pro
12	16	100.0	1302	4	AAD13032	Aad13032 Human-pro
13	16	100.0	1302	4	AAD06750	Aad06750 Human-pro
14	16	100.0	1302	4	AAS11528	Aas11528 Human cDN
15	16	100.0	1302	6	ABL52468	Abl52468 Human-pro
16	16	100.0	1302	12	ADJ94337	Adj94337 Human-pro
17	16	100.0	1302	12	ADO50433	Ado50433 Human-pro
18	16	100.0	1302	13	ADR75346	Adr75346 Human-pro
19	16	100.0	1305	4	AAS11733	Aas11733 DNA encod
20	16	100.0	1305	4	AAD17896	Aad17896 Human-Asp
21	16	100.0	1305	4	AAD13277	Aad13277 Human-Asp
22	16	100.0	1305	4	AAD06769	Aad06769 Human asp
23	16	100.0	1305	4	AAS11548	Aas11548 Human cDN
24	16	100.0	1305	6	ABL52488	Abl52488 Human Asp
25	16	100.0	1305	12	ADJ94364	Adj94364 Human-pro
26	16	100.0	1305	12	ADO50460	Ado50460 Human Asp
27	16	100.0	1305	13	ADR75373	Adr75373 Human Asp
28	16	100.0	1341	3	AAA15668	Aaa15668 T7-caspas
29	16	100.0	1341	4	AAS11711	Aas11711 DNA encod
30	16	100.0	1341	4	AAD17874	Aad17874 T7-Human-
31	16	100.0	1341	4	AAD13030	Aad13030 T7-Human-
32	16	100.0	1341	4	AAD06748	Aad06748 T7-Human-
33	16	100.0	1341	4	AAS11526	Aas11526 Human cDN
34	16	100.0	1341	6	ABL52466	Abl52466 T7-human-
35	16	100.0	1341	12	ADJ94333	Adj94333 Human cDN
36	16	100.0	1341	12	ADO50429	Ado50429 T7-Human-
37	16	100.0	1341	13	ADR75342	Adr75342 T7-Human-
38	16	100.0	1362	3	AAA15688	Aaa15688 Modified
39	16	100.0	1362	4	AAS11715	Aas11715 DNA encod
40	16	100.0	1362	4	AAD17878	Aad17878 Human-Asp
41	16	100.0	1362	4	AAD13034	Aad13034 Human-Asp
42	16	100.0	1362	4	AAD06752	Aad06752 Human-Asp
43	16	100.0	1362	4	AAS11530	Aas11530 Human cDN
44	16	100.0	1362	6	ABL52470	Abl52470 Human Asp
45	16	100.0	1362	12	ADJ94341	Adj94341 Human-pro

ALIGNMENTS

RESULT 1
AAD17895
ID AAD17895 standard; cDNA; 1287 BP.
XX
AC AAD17895;
XX
DT 10-DEC-2001 (first entry)
XX
DE Human-Asp 2(b) protein lacking transmembrane domain encoding cDNA.
XX
KW Human; aspartyl protease 2b; Asp2b; amyloid precursor protein; APP;
KW Alzheimer's disease; AD; dementia; neurofibrillary tangle; gliosis;
KW amyloid plaque; neuronal loss; proteolytic; nootropic; neuroprotective;
KW ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 1. .1287
FT /*tag= a
FT /product= "Human-Asp 2(b) protein lacking transmembrane
FT domain"
XX
PN GB2357767-A.
XX
PD 04-JUL-2001.
XX
PF 22-SEP-2000; 2000GB-00023315.

```
XX
PR   23-SEP-1999;   99US-00404133.
PR   23-SEP-1999;   99US-0155493P.
PR   23-SEP-1999;   99WO-US020881.
PR   13-OCT-1999;   99US-00416901.
PR   06-DEC-1999;   99US-0169232P.
XX
PA   (PHAA ) PHARMACIA & UPJOHN CO.
XX
PI   Bienkowkski MJ,  Gurney M;
XX
DR   WPI; 2001-444208/48.
DR   P-PSDB; AAE10646.
XX
PT   Polypeptide comprising fragments of human aspartyl protease with amyloid
PT   precursor protein processing activity and alpha-secretase activity, for
PT   identifying modulators useful in treating Alzheimer's disease.
XX
PS   Example 10; Page 137; 187pp; English.
XX
CC   The patent discloses human aspartyl protease 1 (hu-Asp1) or modified Asp1
CC   proteins which lack transmembrane domain or amino terminal domain or
CC   cytoplasmic domain and retains alpha-secretase activity and amyloid
CC   protein precursor (APP) processing activity. The proteins of the
CC   invention are useful for assaying hu-Asp1 alpha-secretase activity, which
CC   in turn is useful for identifying modulators of hu-Asp1 alpha-secretase
CC   activity, where modulators that increase hu-Asp1 alpha-secretase activity
CC   are useful for treating Alzheimer's disease (AD) which causes progressive
CC   dementia with consequent formation of amyloid plaques, neurofibrillary
CC   tangles, gliosis and neuronal loss. Hu-Asp1 protease substrate is useful
CC   for assaying hu-Asp1 proteolytic activity, by contacting hu-Asp1 protein
CC   with the substrate under acidic conditions and determining the level of
CC   hu-Asp1 proteolytic activity. The present sequence is a cDNA encoding
CC   human Asp 2(b) protein lacking a transmembrane (TM) domain which is
CC   generated by the deletion of the C-terminal TM domain and intracellular
CC   domains of human Asp 2(b) protein
XX
SQ   Sequence 1287 BP; 271 A; 370 C; 384 G; 262 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                2.64e-06        Length:         1287
Score:                    16.00           Matches:        16
Percent Similarity:       100.00%         Conservative:   0
Best Local Similarity:    100.00%         Mismatches:     0
Query Match:              100.00%         Indels:         0
DB:                       4               Gaps:           0

US-10-726-967A-3 (1-16) x AAD17895 (1-1287)

Qy          1 ThrGlnHisGlyIleArgLeuProLeuArgSerGlyLeuGlyGlyAla 16
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 ACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCC 111

RESULT 2
AAD13276
ID   AAD13276 standard; cDNA; 1287 BP.
XX
AC   AAD13276;
XX
DT   23-OCT-2001  (first entry)
XX
DE   Human-Asp2(b) deltaTM protein cDNA.
XX
KW   Human; aspartyl protease 2b; Asp 2b; beta-amyloid precursor protein; APP;
KW   beta-secretase; Alzheimer's disease; dementia; amyloid plaque; gliosis;
KW   neurofibrillary tangle; neuronal loss; amyloid-beta peptide; nootropic;
KW   neuroprotective; antisense therapy; Asp2(b) deltaTM protein;
KW   gene therapy; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1287
FT                   /*tag=  a
FT                   /product= "Human Asp2(b) deltaTM protein"
XX
PN   WO200150829-A2.
XX
PD   19-JUL-2001.
XX
PF   09-MAY-2001; 2001WO-IB000799.
XX
PR   09-MAY-2001; 2001WO-IB000799.
XX
PA   (BIEN/) BIENKOWSKI M J.
PA   (GURN/) GURNEY M E.
PA   (HEIN/) HEINRIKSON R L.
PA   (PARO/) PARODI L A.
PA   (YANR/) YAN R.
XX
PI   Bienkowski MJ,  Gurney ME,  Heinrikson RL,  Parodi LA,  Yan R;
XX
DR   WPI; 2001-483072/52.
DR   P-PSDB; AAE06891.
XX
PT   Novel purified polypeptide comprising fragment of mammalian aspartyl
PT   protease 2, lacking Asp2 transmembrane domain and retaining beta
PT   secretase activity of Asp2 useful for identifying inhibitors of Asp2
PT   activity.
XX
PS   Example 10; Page 166-167; 185pp; English.
XX
CC   The invention relates to human aspartyl proteases (Hu-Asp), beta-amyloid
CC   precursor protein (APP) isoforms and their corresponding DNA molecules.
CC   Human aspartyl proteases can act as beta-secretase proteases useful for
CC   treating Alzheimer's disease. APP isoforms are useful for identifying
CC   modulators of amyloid-beta peptide production, for use in designing
CC   therapeutics for the treatment and prevention of Alzheimer's disease,
CC   dementia, formation of amyloid plaques, neurofibrillary tangles, gliosis
CC   and neuronal loss. APP isoforms are also used in methods for identifying
CC   inhibitors and modulators of human Asp2 activity. The invention relates
CC   to a method for identifying agents that modulate the activity of human
CC   aspartyl protease Asp2. Amyloid-beta peptides obtained from APP are used
CC   as a means to screen in cellular assays for the inhibitors of beta- and
CC   gamma- secretase. Hu-Asp DNA fragments are useful as probes or primers in
CC   polymerase chain reactions (PCR). The probes are useful for detecting Hu-
CC   Asp nucleic acids in in vitro assays and in Northern and Southern blots.
CC   The present cDNA sequence encodes Human aspartyl protease 2b (Hu-Asp2b)
CC   deltaTM protein which is obtained by the deletion of C-terminal
CC   transmembrane and intracellular domains of Hu-Asp2b. Human Asp2b has beta
CC   -secretase activity
XX
SQ   Sequence 1287 BP; 271 A; 370 C; 384 G; 262 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                2.64e-06        Length:         1287
Score:                    16.00           Matches:        16
Percent Similarity:       100.00%         Conservative:   0
Best Local Similarity:    100.00%         Mismatches:     0
Query Match:              100.00%         Indels:         0
DB:                       4               Gaps:           0

US-10-726-967A-3 (1-16) x AAD13276 (1-1287)

Qy          1 ThrGlnHisGlyIleArgLeuProLeuArgSerGlyLeuGlyGlyAla 16
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 ACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCC 111

RESULT 3
AAD06768
ID   AAD06768 standard; cDNA; 1287 BP.
XX
AC   AAD06768;
XX
DT   10-AUG-2001  (first entry)
```

```
XX
DE   Human aspartyl protease 2 (b) delta TM cDNA.
XX
KW   Human; alpha-secretase; amyloid precursor protein; APP; therapy;
KW   Alzheimer's disease; antialzheimer's; aspartyl protease 2; Asp 2;
KW   beta-secretase; chromosome 11q23.3-24.1; mutant; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1287
FT                   /*tag=  a
FT                   /product= "Human aspartyl protease 2 (b) delta TM"
XX
PN   WO200123533-A2.
XX
PD   05-APR-2001.
XX
PF   22-SEP-2000; 2000WO-US026080.
XX
PR   23-SEP-1999;   99US-0155493P.
PR   23-SEP-1999;   99WO-US020881.
PR   13-OCT-1999;   99US-00416901.
PR   06-DEC-1999;   99US-0169232P.
XX
PA   (PHAA ) PHARMACIA & UPJOHN CO.
XX
PI   Gurney M,  Bienkowski MJ;
XX
DR   WPI; 2001-290516/30.
DR   P-PSDB; AAE02598.
XX
PT   Enzymes that cleave the alpha-secretase site of the amyloid precursor
PT   protein, useful for the treatment of Alzheimer's disease.
XX
PS   Example 10; Page 165-166; 189pp; English.
XX
CC   The present invention relates to enzymes for cleaving the alpha-
CC   secretase site of the amyloid precursor protein (APP) and methods of
CC   identifying those enzymes. The methods may be used to identify enzymes
CC   that may be used to cleave the alpha-secretase cleavage site of the APP
CC   protein. The enzymes may be used to treat or modulate the progress of
CC   Alzheimer's disease. The present sequence is human aspartyl protease 2
CC   (Asp 2) (b) delta TM cDNA. The Asp 2 gene from which it is derived is
CC   located on chromosome 11q23.3-24.1. The Asp 2 has beta-secretase protease
CC   activity
XX
SQ   Sequence 1287 BP; 271 A; 370 C; 384 G; 262 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              2.64e-06        Length:         1287
Score:                  16.00           Matches:        16
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     4               Gaps:           0

US-10-726-967A-3 (1-16) x AAD06768 (1-1287)

Qy          1 ThrGlnHisGlyIleArgLeuProLeuArgSerGlyLeuGlyGlyAla 16
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 ACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCC 111

RESULT 4
AAS11547
ID   AAS11547 standard; cDNA; 1287 BP.
XX
AC   AAS11547;
XX
DT   24-OCT-2001  (first entry)
XX
DE   Human cDNA encoding Human-pro-Asp 2(b) delta TM.
XX
KW   Human; Aspartyl protease; beta-secretase; nootropic; ASP2;
KW   neuroprotective; amyloid protein precursor; APP; Alzheimer's disease;
KW   amyloid-beta; Abeta; Human-pro-Asp 2(b) delta TM; ss; mutant.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1287
FT                   /*tag=  a
FT                   /product= "Human-pro-Asp 2(b) delta TM"
XX
PN   WO200149098-A2.
XX
PD   12-JUL-2001.
XX
PF   09-MAY-2001; 2001WO-IB000798.
XX
PR   09-MAY-2001; 2001WO-IB000798.
XX
PA   (BIEN/) BIENKOWSKI M J.
PA   (GURN/) GURNEY M E.
PA   (HEIN/) HEINRIKSON R L.
PA   (PARO/) PARODI L A.
PA   (YANR/) YAN R.
XX
PI   Bienkowski MJ,  Gurney ME,  Heinrikson RL,  Parodi LA,  Yan R;
XX
DR   WPI; 2001-502549/55.
XX
PT   Novel purified polypeptide comprising fragment of mammalian aspartyl
PT   protease 2, lacking Asp2 transmembrane domain and retaining beta
PT   secretase activity of Asp2 useful for identifying inhibitors of Asp2
PT   activity.
XX
PS   Disclosure; Page 166-167; 185pp; English.
XX
CC   The invention relates to a purified polypeptide comprising a fragment of
CC   mammalian aspartyl protease (Asp)2 protein which lacks the Asp2
CC   transmembrane domain and the Asp2 protein, and where the polypeptide and
CC   the fragment retain the beta-secretase activity of the mammalian Asp2
CC   protein. The invention also details polynucleotides for the Asp proteins
CC   and vectors expressing them, and a polypeptide (isoform of amyloid
CC   protein precursor (APP)) comprising the amino acid sequence of an APP or
CC   its fragment containing an APP cleavage site recognizable by a mammalian
CC   beta-secretase, and further comprising two lysine residues at the
CC   carboxyl terminus of the amino acid sequence of the mammalian APP or APP
CC   fragment. Also included in the invention are methods of identifying
CC   modulators or inhibitors of Asp2. Modulators and inhibitors of Asp2 are
CC   useful for treating Alzheimer's disease. APP is useful in methods for
CC   identifying inhibitors or modulators of human Asp2 activity and amyloid-
CC   beta (Abeta) peptide production. APP is also useful in designing
CC   therapeutics for the treatment or prevention of Alzheimer's disease. APP
CC   comprising the APP-Sw-beta-secretase peptide sequence (NLDA), which is
CC   associated with increased levels of Abeta processing is useful in assays
CC   relating the Alzheimer's research. The expression vector is useful for
CC   recombinantly expressing APP. Nucleic acids that hybridise to Asp
CC   oligonucleotides are useful as probes or primers. The probes are useful
CC   for detecting Hu-Asp nucleic acids in in vitro assays and in Northern and
CC   Southern blots. The present sequence encodes Human-pro- Asp 2(b) delta TM
CC   protein, which lacks the C-terminal transmembrane domain
XX
SQ   Sequence 1287 BP; 271 A; 370 C; 384 G; 262 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              2.64e-06        Length:         1287
Score:                  16.00           Matches:        16
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     4               Gaps:           0
```

US-10-726-967A-3 (1-16) x AAS11547 (1-1287)

```
Qy          1 ThrGlnHisGlyIleArgLeuProLeuArgSerGlyLeuGlyGlyAla 16
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 ACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCC 111
```

RESULT 5
ABL52487
ID ABL52487 standard; cDNA; 1287 BP.
XX
AC ABL52487;
XX
DT 16-JUL-2002 (first entry)
XX
DE Human Asp-2(b)deltaTM nucleotide sequence SEQ ID NO:50.
XX
KW Human; Asp-1; Asp-2; aspartyl protease; Alzheimer's disease; proteolytic;
KW chromosome 11q23.3-24.1; gene; ss.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   1. .1287
FT   /*tag= a
FT   /product= "Human Asp-2(b)delta TM"
XX
PN GB2367060-A.
XX
PD 27-MAR-2002.
XX
PF 29-OCT-2001; 2001GB-00025934.
XX
PR 23-SEP-1999; 99US-00404133.
PR 23-SEP-1999; 99US-0155493P.
PR 23-SEP-1999; 99WO-US020881.
PR 13-OCT-1999; 99US-00416901.
PR 06-DEC-1999; 99US-0169232P.
PR 22-SEP-2000; 2000GB-00023315.
XX
PA (PHAA) PHARMACIA & UPJOHN CO.
XX
PI Bienkowkski MJ, Gurney M;
XX
DR WPI; 2002-397167/43.
DR P-PSDB; ABB78607.
XX
PT Human aspartyl protease 1 substrates useful in assays to detect aspartyl
PT protease activity, e.g. for the diagnosis of Alzheimer's disease.
XX
PS Example 10; Page 137; 182pp; English.
XX
CC The present invention describes a human aspartyl protease 1 (hu-Asp1)
CC substrate (I) which comprises a peptide of no more than 50 amino acids,
CC and which comprises the 8 amino acid sequence Gly-Leu-Ala-Leu-Ala-Leu-
CC Glu-Pro. Also described are: (1) a method (II) for assaying hu-Asp1
CC proteolytic activity, comprising: (a) contacting a hu-Asp1 protein with
CC (I) under acidic conditions; and (b) determining the level of hu-Asp1
CC proteolytic activity; (2) a purified polynucleotide (III) comprising a
CC nucleotide sequence that hybridises under stringent conditions to the non
CC -coding strand complementary to a defined 1804 nucleotide sequence (see
CC ABL52456) where the nucleotide sequence encodes a polypeptide having Asp1
CC proteolytic activity and lacks nucleotides encoding a transmembrane
CC domain); (3) a purified polynucleotide (III') comprising a sequence that
CC hybridises under stringent conditions to (III) (the nucleotide sequence
CC encodes a polypeptide further lacking a pro-peptide domain corresponding
CC to amino acids 23-62 of hu-Asp1 (see ABB78589)); (4) a vector (IV)
CC comprising (III) or (III'); and (5) a host cell (V) transformed or
CC transfected with (III), (III') and/or (IV). The hu-Asp1 protease
CC substrate (I) may be used as an enzyme substrate in assays to detect
CC aspartyl protease activity, (II) and therefore diagnose diseases
CC associated with aberrant hu-Asp1 expression and activity such as
CC Alzheimer's disease. Hu-Asp1 has been localised to chromosome 21, while
CC hu-Asp2 has been localised to chromosome 11q23.3-24.1. The present
CC sequence encodes human Asp-2(b)deltaTM, which is given in an example from
CC the present invention
XX
SQ Sequence 1287 BP; 271 A; 370 C; 384 G; 262 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	2.64e-06	Length:	1287
Score:	16.00	Matches:	16
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0

US-10-726-967A-3 (1-16) x ABL52487 (1-1287)

```
Qy          1 ThrGlnHisGlyIleArgLeuProLeuArgSerGlyLeuGlyGlyAla 16
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 ACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCC 111
```

RESULT 6
ADJ94362
ID ADJ94362 standard; cDNA; 1287 BP.
XX
AC ADJ94362;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human-pro-Asp-2(b)deltaTM cDNA.
XX
KW Human; ss; gene; aspartyl protease; Asp-1; Asp-2(a); Asp-2(b);
KW beta secretase; amyloid protein precursor; APP; Alzheimer's disease;
KW nootropic; neuroprotective; amyloid beta; mutant.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN US6706485-B1.
XX
PD 16-MAR-2004.
XX
PF 12-APR-2000; 2000US-00548376.
XX
PR 24-SEP-1998; 98US-0101594P.
PR 23-SEP-1999; 99US-00404133.
PR 23-SEP-1999; 99US-0155493P.
PR 23-SEP-1999; 99WO-US020881.
PR 13-OCT-1999; 99US-00416901.
XX
PA (PHAA) PHARMACIA & UPJOHN CO.
XX
PI Gurney ME, Bienkowski MJ, Heinrikson RL, Parodi LA, Yan R;
XX
DR WPI; 2004-236722/22.
DR P-PSDB; ADJ94363.
XX
PT Identifying agents that modulate activity of Asp2 aspartyl protease
PT useful for treating or preventing Alzheimer's disease involves comparing
PT APP processing activity of protease in presence and absence of test
PT agent.
XX
PS Example 10; SEQ ID NO 50; 109pp; English.
XX
CC The invention relates to identifying agents that modulate activity of
CC Asp2 (e.g. a beta-secretase, e.g. human Asp-2(b) appearing as ID 6,
CC encoded by ID 5) aspartyl protease, involves contacting Asp2 with amyloid
CC precursor protein (APP) in the presence and absence of a test agent,
CC where Asp2 is a recombinant polypeptide and processes APP into amyloid
CC beta, determining APP processing activity of Asp2 in presence and absence
CC of the test agent, and comparing the activities to identify agents that
CC modulate the activity of Asp2. Also disclosed are the cDNA and proteins
CC for human Asp-1 and Asp-2(a), mouse Asp-2(b), a vector comprising the
CC nucleic acid encoding Hu-Asp2 protease sequence, a host cell comprising
CC the vector and the method of producing Hu-Asp polypeptide, an isolated

```
CC   antibody that specifically binds to Hu-Asp polypeptides, identifying a
CC   cell that can be used to screen for inhibitors of beta secretase
CC   activity, novel isoforms of amyloid protein precursor (APP), where the
CC   last 2 carboxy terminus amino acids of that isoform are both lysine
CC   residues (e.g. those designated APP695-KK or carrying the Swedish
CC   mutation where KM at 595-596 is mutated to NL, designated e.g. APP695-Sw
CC   or APP695-Sw-KK, or a V to F mutation at 642, e.g. APP695-VF, all useful
CC   for assaying for beta secretase activity and screening for inhibitors of
CC   beta-secretase) and polynucleotides that encode the APP proteins. The
CC   method is useful for identifying agents that modulate the activity
CC   (amyloid precursor protein processing activity) of Asp2 aspartyl
CC   protease. Preferably, the method is useful for identifying agents that
CC   inhibit Asp2 aspartyl protease activity. The inhibitors of amyloid
CC   precursor protein processing, are useful for treating or preventing
CC   Alzheimer's disease. The present sequence encodes an aspartyl protease
CC   mutant construct (e.g. lacking a transmembrane domain and/or including a
CC   caspase cleavage site) used to investigate the cleavage activity of Asp2
CC   proteins.
XX
SQ   Sequence 1287 BP; 271 A; 370 C; 384 G; 262 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              2.64e-06      Length:          1287
Score:                  16.00         Matches:         16
Percent Similarity:     100.00%       Conservative:    0
Best Local Similarity:  100.00%       Mismatches:      0
Query Match:            100.00%       Indels:          0
DB:                     12            Gaps:            0

US-10-726-967A-3 (1-16) x ADJ94362 (1-1287)

Qy          1 ThrGlnHisGlyIleArgLeuProLeuArgSerGlyLeuGlyGlyAla 16
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 ACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCC 111

RESULT 7
ADO50458
ID   ADO50458 standard; DNA; 1287 BP.
XX
AC   ADO50458;
XX
DT   29-JUL-2004  (first entry)
XX
DE   Human Asp2(b)deltaTM mutant DNA.
XX
KW   Aspartyl protease; Asp; beta secretase; amyloid precursor protein; APP;
KW   Alzheimer's disease; gene therapy; human; mutant; gene; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1287
FT                   /*tag=  a
FT                   /product= "Human Asp2(b) mutant protein"
XX
PN   US6737510-B1.
XX
PD   18-MAY-2004.
XX
PF   12-APR-2000; 2000US-00548373.
XX
PR   24-SEP-1998;   98US-0101594P.
PR   23-SEP-1999;   99US-00404133.
PR   23-SEP-1999;   99US-0155493P.
PR   23-SEP-1999;   99WO-US020881.
PR   13-OCT-1999;   99US-00416901.
XX
PA   (PHAA ) PHARMACIA & UPJOHN CO.
XX
PI   Gurney ME,  Bienkowski MJ,  Heinrikson RL,  Parodi LA,  Yan R;
XX
DR   WPI; 2004-387112/36.
DR   P-PSDB; ADO50459.
XX
PT   New Asp2 aspartyl protease protein comprising tripeptides DTG and DSG
PT   involved in processing amyloid precursor protein into amyloid beta,
PT   useful in preparing a composition for treating or preventing Alzheimer's
PT   disease.
XX
PS   Example 10; SEQ ID NO 50; 108pp; English.
XX
CC   The invention relates to a method for identifying an agent that decreases
CC   the protease activity of the aspartyl protease (Asp) polypeptide. It also
CC   provides enzyme and enzymatic procedures for cleaving the beta secretase
CC   cleavage site of the amyloid precursor protein (APP). The invention is
CC   useful in preparing a composition for treating or preventing Alzheimer's
CC   disease. It is also useful in gene therapy. The present sequence is human
CC   Asp2(b) mutant DNA. This sequence is used to illustrate the method of the
CC   invention.
XX
SQ   Sequence 1287 BP; 271 A; 370 C; 384 G; 262 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              2.64e-06      Length:          1287
Score:                  16.00         Matches:         16
Percent Similarity:     100.00%       Conservative:    0
Best Local Similarity:  100.00%       Mismatches:      0
Query Match:            100.00%       Indels:          0
DB:                     12            Gaps:            0

US-10-726-967A-3 (1-16) x ADO50458 (1-1287)

Qy          1 ThrGlnHisGlyIleArgLeuProLeuArgSerGlyLeuGlyGlyAla 16
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 ACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCC 111

RESULT 8
ADR75371
ID   ADR75371 standard; DNA; 1287 BP.
XX
AC   ADR75371;
XX
DT   18-NOV-2004  (first entry)
XX
DE   Human Asp2(b)deltaTM mutant DNA.
XX
KW   Aspartyl protease; Asp; amyloid precursor protein; APP; amyloid beta;
KW   chromosome identification; Alzheimer's disease; human; mutant; gene; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1287
FT                   /*tag=  a
FT                   /product= "Human Asp2(b) mutant protein"
XX
PN   US2004166507-A1.
XX
PD   26-AUG-2004.
XX
PF   29-AUG-2003; 2003US-00652045.
XX
PR   24-SEP-1998;   98US-0101594P.
PR   23-SEP-1999;   99US-00404133.
PR   23-SEP-1999;   99US-0155493P.
PR   13-OCT-1999;   99US-00416901.
XX
PA   (GURN/) GURNEY M E.
PA   (BIEN/) BIENKOWAKI M J.
PA   (HEIN/) HEINRIKSON R L.
PA   (PARO/) PARODI L A.
PA   (YANR/) YAN R.
XX
PI   Gurney ME,  Bienkowaki MJ,  Heinrikson RL,  Parodi LA,  Yan R;
```

```
XX
DR   WPI; 2004-624916/60.
DR   P-PSDB; ADR75372.
XX
PT   Novel purified/isolated polynucleotide encoding polypeptide having
PT   aspartyl protease activity involved in processing amyloid precursor
PT   protein into amyloid beta, useful in identifying agent decreasing
PT   activity of aspartyl protease.
XX
PS   Example 10; SEQ ID NO 50; 107pp; English.
XX
CC   The invention relates to nucleic acid sequences encoding aspartyl
CC   protease (Asp) polypeptides having aspartyl protease activity involved in
CC   processing amyloid precursor protein (APP) into amyloid beta. The
CC   invention also relates to a method for identifying an agent that
CC   decreases the protease activity of the Asp. Asp DNA is useful in
CC   chromosome identification as they can hybridise with a specific location
CC   on a human chromosome and in identifying the relationship between genes
CC   and diseases (particular gene responsible for causing diseases). It is
CC   also useful for identifying candidates to modulate the progression of
CC   Alzheimer's disease. Asp is useful in raising antibodies that are useful
CC   in diagnostic assay for detecting Hu-Asp polypeptide expression. The
CC   present sequence is the human Asp2(b)deltaTM mutant DNA. This sequence is
CC   used to illustrate the method of the invention.
XX
SQ   Sequence 1287 BP; 271 A; 370 C; 384 G; 262 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                2.64e-06        Length:         1287
Score:                    16.00           Matches:        16
Percent Similarity:       100.00%         Conservative:   0
Best Local Similarity:    100.00%         Mismatches:     0
Query Match:              100.00%         Indels:         0
DB:                       13              Gaps:           0

US-10-726-967A-3 (1-16) x ADR75371 (1-1287)

Qy          1 ThrGlnHisGlyIleArgLeuProLeuArgSerGlyLeuGlyGlyAla 16
              ||||||||||||||||||||||||||||||||
Db         64 ACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCC 111

RESULT 9
AAA15670
ID   AAA15670 standard; DNA; 1302 BP.
XX
AC   AAA15670;
XX
DT   15-SEP-2003  (revised)
DT   06-AUG-2003  (revised)
DT   03-AUG-2000  (first entry)
XX
DE   Human-pro-Asp-2(a)-deltaTM nucleotide sequence.
XX
KW   Aspartyl protease; aspartase; amyloid precursor protein; APP; Asp 2; ss;
KW   Alzheimer's disease; beta secretase site; human-pro-Asp-2(a)-deltaTM.
XX
OS   Homo sapiens.
OS   Enterobacteria phage T7.
OS   Chimeric.
XX
PN   WO200017369-A2.
XX
PD   30-MAR-2000.
XX
PF   23-SEP-1999;   99WO-US020881.
XX
PR   24-SEP-1998;   98US-0101594P.
XX
PA   (PHAA ) PHARMACIA & UPJOHN CO.
XX
PI   Gurney ME,  Bienkowski MJ,  Heinrikson RL,  Parodi LA,  Yan R;
XX
DR   WPI; 2000-303209/26.
DR   P-PSDB; AAY88433.
XX
PT   New enzyme designated human aspartase useful in research into Alzheimer's
PT   Disease is capable of cleaving amyloid protein precursor at the beta
PT   secretase site to produce amyloid beta peptide.
XX
PS   Example 9; Fig 8; 183pp; English.
XX
CC   This sequence represents a modified version of the human aspartase 2
CC   (Asp2) nucleotide sequence. The sequence is used in the bacterial
CC   expression of human Asp2L. The invention relates to a protease (e.g.
CC   Asp2) capable of cleaving the beta secretase site of amyloid precursor
CC   protein (APP). The protease contains a sequence encoding the amino acid
CC   sequence DTG and a sequence encoding DSG or DTG separated by 100-300
CC   amino acids. When mutated the APP gene causes an autosomal dominant form
CC   of Alzheimer's disease. APP localises to the cell surface membrane and
CC   have a single C-terminal transmembrane domain. Proteolytic processing of
CC   APP produces the amyloid beta protein, which is possibly very important
CC   in Alzheimer's disease. The invention includes a nucleotide sequence
CC   encoding the protease, a vector containing the nucleotide sequence, and a
CC   cell line comprising the vector. Methods for screening for inhibitors of
CC   beta secretase activity are also given in the invention. The human
CC   aspartase protein and nucleotide sequences and the methods for
CC   identifying inhibitors of the protease, are useful in the treatment of
CC   and research in to Alzheimer's disease. (Updated on 06-AUG-2003 to
CC   correct OS field.) (Updated on 15-SEP-2003 to standardise OS field)
XX
SQ   Sequence 1302 BP; 281 A; 367 C; 370 G; 284 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                2.67e-06        Length:         1302
Score:                    16.00           Matches:        16
Percent Similarity:       100.00%         Conservative:   0
Best Local Similarity:    100.00%         Mismatches:     0
Query Match:              100.00%         Indels:         0
DB:                       3               Gaps:           0

US-10-726-967A-3 (1-16) x AAA15670 (1-1302)

Qy          1 ThrGlnHisGlyIleArgLeuProLeuArgSerGlyLeuGlyGlyAla 16
              ||||||||||||||||||||||||||||||||
Db          4 ACTCAGCATGGTATTCGTCTGCCACTGCGTAGCGGTCTGGGTGGTGCT 51

RESULT 10
AAS11713
ID   AAS11713 standard; DNA; 1302 BP.
XX
AC   AAS11713;
XX
DT   11-SEP-2003  (revised)
DT   24-OCT-2001  (first entry)
XX
DE   DNA encoding T7-human aspartyl protease 2a deltaTM (low GC).
XX
KW   Human; aspartyl protease 1; Asp-1; nootropic; neuroprotective;
KW   aspartyl protease 2; Asp2; amyloid protein precursor; APP;
KW   beta-secretase; Alzheimer's disease; ds.
XX
OS   Homo sapiens.
OS   Enterobacteria phage T7.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1302
FT                   /*tag=  a
FT                   /product= "T7-Aspartyl protease-2a delta TM (low GC)"
XX
PN   WO200149097-A2.
XX
PD   12-JUL-2001.
XX
PF   09-MAY-2001; 2001WO-IB000797.
XX
PR   09-MAY-2001; 2001WO-IB000797.
```

```
XX
PA   (BIEN/) BIENKOWSKI M J.
PA   (GURN/) GURNEY M E.
PA   (HEIN/) HEINRIKSON R L.
PA   (PARO/) PARODI L A.
PA   (YANR/) YAN R.
XX
PI   Bienkowski MJ,  Gurney ME,  Heinrikson RL,  Parodi LA,  Yan R;
XX
DR   WPI; 2001-502548/55.
DR   P-PSDB; AAU07113.
XX
PT   Novel purified polypeptide comprising fragment of mammalian aspartyl
PT   protease 2, lacking Asp2 transmembrane domain and retaining beta
PT   secretase activity of Asp2 useful for identifying inhibitors of Asp2
PT   activity.
XX
PS   Example 9; Fig 8; 185pp; English.
XX
CC   The invention relates to a novel purified polypeptide comprising a
CC   fragment of mammalian aspartyl protease 2 (Asp2) protein which lacks the
CC   Asp2 transmembrane domain and the Asp2 protein, and where the polypeptide
CC   and the fragment retain the beta-secretase activity of the mammalian Asp2
CC   protein. Also included is an isoform of amyloid protein precursor (APP)
CC   comprising the amino acid sequence of a APP or its fragment containing an
CC   APP cleavage site recognisable by a mammalian beta-secretase, and further
CC   comprising two lysine residues at the carboxyl terminus of the amino acid
CC   sequence of the mammalian APP or APP fragment. The polypeptides are used
CC   for assaying for modulators of beta-secretase activity; identifying
CC   agents that inhibit the APP processing activity of human Asp2 aspartyl
CC   protease (Hu-Asp2); identifying agents that modulate the activity of Asp2
CC   ; and for reducing cellular production of amyloid beta (Abeta) from APP.
CC   Agents identified by the above methods are useful for treating
CC   Alzheimer's disease; for identifying modulators of amyloid-beta (Abeta)
CC   peptide production, and for use in designing therapeutics for the
CC   treatment or prevention of Alzheimer's disease. Probes and primers
CC   derived from Asp nucleic acid sequences are useful for detecting Hu-Asp
CC   nucleic acids in in vitro assays and in Northern and Southern blots. The
CC   present sequence represents the coding sequence of T7-human Asp-2a delta
CC   TM (low GC) construct which has a T7 tag, has the GC content of the 5'
CC   sequence reduced by site-directed mutagenesis, and lacks the
CC   transmembrane domain. This construct was used for bacterial expression
CC   and purification of human Asp2a. (Updated on 11-SEP-2003 to standardise
CC   OS field)
XX
SQ   Sequence 1302 BP; 281 A; 367 C; 370 G; 284 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              2.67e-06        Length:         1302
Score:                  16.00           Matches:        16
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     4               Gaps:           0

US-10-726-967A-3 (1-16) x AAS11713 (1-1302)

Qy          1 ThrGlnHisGlyIleArgLeuProLeuArgSerGlyLeuGlyGlyAla 16
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db          4 ACTCAGCATGGTATTCGTCTGCCACTGCGTAGCGGTCTGGGTGGTGCT 51

RESULT 11
AAD17876
ID   AAD17876 standard; cDNA; 1302 BP.
XX
AC   AAD17876;
XX
DT   10-DEC-2001  (first entry)
XX
DE   Human-pro-Asp 2(a) protein lacking TM domain (low GC) encoding cDNA.
XX
KW   Human; aspartyl protease 1; Aspl; amyloid precursor protein; APP;
KW   Alzheimer's disease; AD; dementia; neurofibrillary tangle; gliosis;
KW   amyloid plaque; neuronal loss; proteolytic; nootropic; neuroprotective;
KW   Human-pro-Asp 2(a) protein; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1302
FT                   /*tag= a
FT                   /product= "Human-pro-Asp 2(a) protein lacking
FT                   transmembrane domain"
XX
PN   GB2357767-A.
XX
PD   04-JUL-2001.
XX
PF   22-SEP-2000; 2000GB-00023315.
XX
PR   23-SEP-1999;   99US-00404133.
PR   23-SEP-1999;   99US-0155493P.
PR   23-SEP-1999;   99WO-US020881.
PR   13-OCT-1999;   99US-00416901.
PR   06-DEC-1999;   99US-0169232P.
XX
PA   (PHAA ) PHARMACIA & UPJOHN CO.
XX
PI   Bienkowkski MJ,  Gurney M;
XX
DR   WPI; 2001-444208/48.
DR   P-PSDB; AAE10640.
XX
PT   Polypeptide comprising fragments of human aspartyl protease with amyloid
PT   precursor protein processing activity and alpha-secretase activity, for
PT   identifying modulators useful in treating Alzheimer's disease.
XX
PS   Example 9; Fig 8; 187pp; English.
XX
CC   The patent discloses human aspartyl protease 1 (hu-Asp1) or modified Asp1
CC   proteins which lack transmembrane domain or amino terminal domain or
CC   cytoplasmic domain and retains alpha-secretase activity and amyloid
CC   protein precursor (APP) processing activity. The proteins of the
CC   invention are useful for assaying hu-Asp1 alpha-secretase activity, which
CC   in turn is useful for identifying modulators of hu-Asp1 alpha-secretase
CC   activity, where modulators that increase hu-Asp1 alpha-secretase activity
CC   are useful for treating Alzheimer's disease (AD) which causes progressive
CC   dementia with consequent formation of amyloid plaques, neurofibrillary
CC   tangles, gliosis and neuronal loss. Hu-Asp1 protease substrate is useful
CC   for assaying hu-Asp1 proteolytic activity, by contacting hu-Asp1 protein
CC   with the substrate under acidic conditions and determining the level of
CC   hu-Asp1 proteolytic activity. The present sequence is a cDNA encoding
CC   human-pro-Asp 2(a) protein lacking a transmembrane (TM) domain (low GC)
CC   which is generated from human Asp 2(a) protein by the deletion of its C-
CC   terminal transmembrane domain and change of degenerate codons bases in 15
CC   amino acid positions from G/C to A/T to reduce the GC content
XX
SQ   Sequence 1302 BP; 281 A; 367 C; 370 G; 284 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              2.67e-06        Length:         1302
Score:                  16.00           Matches:        16
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     4               Gaps:           0

US-10-726-967A-3 (1-16) x AAD17876 (1-1302)

Qy          1 ThrGlnHisGlyIleArgLeuProLeuArgSerGlyLeuGlyGlyAla 16
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db          4 ACTCAGCATGGTATTCGTCTGCCACTGCGTAGCGGTCTGGGTGGTGCT 51

RESULT 12
AAD13032
```

```
ID   AAD13032 standard; cDNA; 1302 BP.
XX
AC   AAD13032;
XX
DT   23-OCT-2001  (first entry)
XX
DE   Human-pro-Asp2(a) deltaTM (low GC) protein cDNA.
XX
KW   Human; aspartyl protease 2a; Asp 2a; beta-amyloid precursor protein; APP;
KW   beta-secretase; Alzheimer's disease; dementia; amyloid plaque; gliosis;
KW   neurofibrillary tangle; neuronal loss; amyloid-beta peptide; nootropic;
KW   neuroprotective; antisense therapy; pro-Asp2(a) deltaTM protein;
KW   gene therapy; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1302
FT                   /*tag=  a
FT                   /product= "Human-pro-Asp2(a) deltaTM (low GC) protein"
XX
PN   WO200150829-A2.
XX
PD   19-JUL-2001.
XX
PF   09-MAY-2001; 2001WO-IB000799.
XX
PR   09-MAY-2001; 2001WO-IB000799.
XX
PA   (BIEN/) BIENKOWSKI M J.
PA   (GURN/) GURNEY M E.
PA   (HEIN/) HEINRIKSON R L.
PA   (PARO/) PARODI L A.
PA   (YANR/) YAN R.
XX
PI   Bienkowski MJ,  Gurney ME,  Heinrikson RL,  Parodi LA,  Yan R;
XX
DR   WPI; 2001-483072/52.
DR   P-PSDB; AAE06870.
XX
PT   Novel purified polypeptide comprising fragment of mammalian aspartyl
PT   protease 2, lacking Asp2 transmembrane domain and retaining beta
PT   secretase activity of Asp2 useful for identifying inhibitors of Asp2
PT   activity.
XX
PS   Example 9; Fig 8; 185pp; English.
XX
CC   The invention relates to human aspartyl proteases (Hu-Asp), beta-amyloid
CC   precursor protein (APP) isoforms and their corresponding DNA molecules.
CC   Human aspartyl proteases can act as beta-secretase proteases useful for
CC   treating Alzheimer's disease. APP isoforms are useful for identifying
CC   modulators of amyloid-beta peptide production, for use in designing
CC   therapeutics for the treatment and prevention of Alzheimer's disease,
CC   dementia, formation of amyloid plaques, neurofibrillary tangles, gliosis
CC   and neuronal loss. APP isoforms are also used in methods for identifying
CC   inhibitors and modulators of human Asp2 activity. The invention relates
CC   to a method for identifying agents that modulate the activity of human
CC   aspartyl protease Asp2. Amyloid-beta peptides obtained from APP are used
CC   as a means to screen in cellular assays for the inhibitors of beta- and
CC   gamma- secretase. Hu-Asp DNA fragments are useful as probes or primers in
CC   polymerase chain reactions (PCR). The probes are useful for detecting Hu-
CC   Asp nucleic acids in in vitro assays and in Northern and Southern blots.
CC   The present cDNA sequence encodes Human-pro-aspartyl protease 2a (Asp2a)
CC   deltaTM (low GC) protein which is obtained by the deletion of C-terminal
CC   transmembrane domain and change of degenerate codons bases in 15 amino
CC   acid positions from G/C to A/T in the Hu-Asp2a. Human Asp2a has beta-
CC   secretase activity
XX
SQ   Sequence 1302 BP; 281 A; 367 C; 370 G; 284 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              2.67e-06        Length:         1302
Score:                  16.00           Matches:        16
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     4               Gaps:           0

US-10-726-967A-3 (1-16) x AAD13032 (1-1302)

Qy          1 ThrGlnHisGlyIleArgLeuProLeuArgSerGlyLeuGlyGlyAla 16
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db          4 ACTCAGCATGGTATTCGTCTGCCACTGCGTAGCGGTCTGGGTGGTGCT 51

RESULT 13
AAD06750
ID   AAD06750 standard; cDNA; 1302 BP.
XX
AC   AAD06750;
XX
DT   10-AUG-2001  (first entry)
XX
DE   Human-pro-Asp-2(a) deltaTM protein cDNA.
XX
KW   Human; alpha-secretase; amyloid precursor protein; APP; therapy;
KW   Alzheimer's disease; antialzheimer's; aspartyl protease 2a; Asp2a;
KW   beta-secretase; Asp-2a delta TM; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1302
FT                   /*tag=  a
FT                   /product= "Human-pro-Asp-2(a) delta TM protein"
XX
PN   WO200123533-A2.
XX
PD   05-APR-2001.
XX
PF   22-SEP-2000; 2000WO-US026080.
XX
PR   23-SEP-1999;   99US-0155493P.
PR   23-SEP-1999;   99WO-US020881.
PR   13-OCT-1999;   99US-00416901.
PR   06-DEC-1999;   99US-0169232P.
XX
PA   (PHAA ) PHARMACIA & UPJOHN CO.
XX
PI   Gurney M,  Bienkowski MJ;
XX
DR   WPI; 2001-290516/30.
DR   P-PSDB; AAE02592.
XX
PT   Enzymes that cleave the alpha-secretase site of the amyloid precursor
PT   protein, useful for the treatment of Alzheimer's disease.
XX
PS   Example 9; Page 155; 189pp; English.
XX
CC   The present invention relates to enzymes for cleaving the alpha-
CC   secretase site of the amyloid precursor protein (APP) and methods of
CC   identifying those enzymes. The methods may be used to identify enzymes
CC   that may be used to cleave the alpha-secretase cleavage site of the APP
CC   protein. The enzymes may be used to treat or modulate the progress of
CC   Alzheimer's disease. The present sequence is a cDNA encoding human
CC   Aspartyl protease 2a (Asp-2a) deltaTM protein which is obtained by
CC   deleting the transmembrane domain and adding a T7 tag at the N-terminal
CC   end. This sequence has beta-secretase protease activity. Note: The
CC   present sequence is also shown in figure 8 of the specification, but
CC   lacks nucleotides at its 3' end. This sequence shown in figure 8 has a
CC   stop codon at its 3' end
XX
SQ   Sequence 1302 BP; 281 A; 367 C; 370 G; 284 T; 0 U; 0 Other;

Alignment Scores:
```

```
Pred. No.:              2.67e-06        Length:         1302
Score:                  16.00           Matches:        16
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     4               Gaps:           0

US-10-726-967A-3 (1-16) x AAD06750 (1-1302)

Qy          1 ThrGlnHisGlyIleArgLeuProLeuArgSerGlyLeuGlyGlyAla 16
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db          4 ACTCAGCATGGTATTCGTCTGCCACTGCGTAGCGGTCTGGGTGGTGCT 51

RESULT 14
AAS11528
ID   AAS11528 standard; cDNA; 1302 BP.
XX
AC   AAS11528;
XX
DT   24-OCT-2001  (first entry)
XX
DE   Human cDNA encoding Human-pro-Asp 2(a) delta TM (low GC).
XX
KW   Human; Aspartyl protease; beta-secretase; nootropic; ASP2;
KW   neuroprotective; amyloid protein precursor; APP; Alzheimer's disease;
KW   amyloid-beta; Abeta; ss; Human-pro-Asp 2(a) delta TM (low GC).
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1302
FT                   /*tag=  a
FT                   /product= "Human-pro-Asp 2(a) delta TM (low GC)"
XX
PN   WO200149098-A2.
XX
PD   12-JUL-2001.
XX
PF   09-MAY-2001; 2001WO-IB000798.
XX
PR   09-MAY-2001; 2001WO-IB000798.
XX
PA   (BIEN/) BIENKOWSKI M J.
PA   (GURN/) GURNEY M E.
PA   (HEIN/) HEINRIKSON R L.
PA   (PARO/) PARODI L A.
PA   (YANR/) YAN R.
XX
PI   Bienkowski MJ,  Gurney ME,  Heinrikson RL,  Parodi LA,  Yan R;
XX
DR   WPI; 2001-502549/55.
DR   P-PSDB; AAU06614.
XX
PT   Novel purified polypeptide comprising fragment of mammalian aspartyl
PT   protease 2, lacking Asp2 transmembrane domain and retaining beta
PT   secretase activity of Asp2 useful for identifying inhibitors of Asp2
PT   activity.
XX
PS   Example 9; Fig 8; 185pp; English.
XX
CC   The invention relates to a purified polypeptide comprising a fragment of
CC   mammalian aspartyl protease (Asp)2 protein which lacks the Asp2
CC   transmembrane domain and the Asp2 protein, and where the polypeptide and
CC   the fragment retain the beta-secretase activity of the mammalian Asp2
CC   protein. The invention also details polynucleotides for the Asp proteins
CC   and vectors expressing them, and a polypeptide (isoform of amyloid
CC   protein precursor (APP)) comprising the amino acid sequence of an APP or
CC   its fragment containing an APP cleavage site recognizable by a mammalian
CC   beta-secretase, and further comprising two lysine residues at the
CC   carboxyl terminus of the amino acid sequence of the mammalian APP or APP
CC   fragment. Also included in the invention are methods of identifying
CC   modulators or inhibitors of Asp2. Modulators and inhibitors of Asp2 are
CC   useful for treating Alzheimer's disease. APP is useful in methods for
CC   identifying inhibitors or modulators of human Asp2 activity and amyloid-
CC   beta (Abeta) peptide production. APP is also useful in designing
CC   therapeutics for the treatment or prevention of Alzheimer's disease. APP
CC   comprising the APP-Sw-beta-secretase peptide sequence (NLDA), which is
CC   associated with increased levels of Abeta processing is useful in assays
CC   relating the Alzheimer's research. The expression vector is useful for
CC   recombinantly expressing APP. Nucleic acids that hybridise to Asp
CC   oligonucleotides are useful as probes or primers. The probes are useful
CC   for detecting Hu-Asp nucleic acids in in vitro assays and in Northern and
CC   Southern blots. The present sequence encodes Human-pro-Asp 2(a) delta TM
CC   (low GC), a synthetic version of Asp 2(a) whose GC content has been
CC   altered to facilitate expression in E.coli
XX
SQ   Sequence 1302 BP; 281 A; 367 C; 370 G; 284 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              2.67e-06        Length:         1302
Score:                  16.00           Matches:        16
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     4               Gaps:           0

US-10-726-967A-3 (1-16) x AAS11528 (1-1302)

Qy          1 ThrGlnHisGlyIleArgLeuProLeuArgSerGlyLeuGlyGlyAla 16
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db          4 ACTCAGCATGGTATTCGTCTGCCACTGCGTAGCGGTCTGGGTGGTGCT 51

RESULT 15
ABL52468
ID   ABL52468 standard; cDNA; 1302 BP.
XX
AC   ABL52468;
XX
DT   16-JUL-2002  (first entry)
XX
DE   Human-pro-Asp-2(a)deltaTM (low GC) nucleotide sequence SEQ ID NO:25.
XX
KW   Human; Asp-1; Asp-2; aspartyl protease; Alzheimer's disease; proteolytic;
KW   amyloid precursor protein; APP; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1302
FT                   /*tag=  a
FT                   /product= "human-pro-Asp-2(a)deltaTM (low GC)"
XX
PN   GB2367060-A.
XX
PD   27-MAR-2002.
XX
PF   29-OCT-2001; 2001GB-00025934.
XX
PR   23-SEP-1999;   99US-00404133.
PR   23-SEP-1999;   99US-0155493P.
PR   23-SEP-1999;   99WO-US020881.
PR   13-OCT-1999;   99US-00416901.
PR   06-DEC-1999;   99US-0169232P.
PR   22-SEP-2000; 2000GB-00023315.
XX
PA   (PHAA ) PHARMACIA & UPJOHN CO.
XX
PI   Bienkowkski MJ,  Gurney M;
XX
DR   WPI; 2002-397167/43.
DR   P-PSDB; ABB78601.
XX
PT   Human aspartyl protease 1 substrates useful in assays to detect aspartyl
PT   protease activity, e.g. for the diagnosis of Alzheimer's disease.
XX
```

PS Example 9; Fig 8; 182pp; English.
XX
CC The present invention describes a human aspartyl protease 1 (hu-Asp1)
CC substrate (I) which comprises a peptide of no more than 50 amino acids,
CC and which comprises the 8 amino acid sequence Gly-Leu-Ala-Leu-Ala-Leu-
CC Glu-Pro. Also described are: (1) a method (II) for assaying hu-Asp1
CC proteolytic activity, comprising: (a) contacting a hu-Asp1 protein with
CC (I) under acidic conditions; and (b) determining the level of hu-Asp1
CC proteolytic activity; (2) a purified polynucleotide (III) comprising a
CC nucleotide sequence that hybridises under stringent conditions to the non
CC -coding strand complementary to a defined 1804 nucleotide sequence (see
CC ABL52456) where the nucleotide sequence encodes a polypeptide having Asp1
CC proteolytic activity and lacks nucleotides encoding a transmembrane
CC domain); (3) a purified polynucleotide (III') comprising a sequence that
CC hybridises under stringent conditions to (III) (the nucleotide sequence
CC encodes a polypeptide further lacking a pro-peptide domain corresponding
CC to amino acids 23-62 of hu-Asp1 (see ABB78589)); (4) a vector (IV)
CC comprising (III) or (III'); and (5) a host cell (V) transformed or
CC transfected with (III), (III') and/or (IV). The hu-Asp1 protease
CC substrate (I) may be used as an enzyme substrate in assays to detect
CC aspartyl protease activity, (II) and therefore diagnose diseases
CC associated with aberrant hu-Asp1 expression and activity such as
CC Alzheimer's disease. Hu-Asp1 has been localised to chromosome 21, while
CC hu-Asp2 has been localised to chromosome 11q23.3-24.1. The present
CC sequence encodes human-pro-Asp-2(a)deltaTM (low GC), which is given in an
CC example from the present invention
XX
SQ Sequence 1302 BP; 281 A; 367 C; 370 G; 284 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	2.67e-06	Length:	1302
Score:	16.00	Matches:	16
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0

US-10-726-967A-3 (1-16) x ABL52468 (1-1302)

```
Qy          1 ThrGlnHisGlyIleArgLeuProLeuArgSerGlyLeuGlyGlyAla 16
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db          4 ACTCAGCATGGTATTCGTCTGCCACTGCGTAGCGGTCTGGGTGGTGCT 51
```

Search completed: July 27, 2005, 19:10:44
Job time : 434 secs

GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: July 27, 2005, 18:52:49 ; Search time 134 Seconds
(without alignments)
195.376 Million cell updates/sec

Title: US-10-726-967A-3
Perfect score: 16
Sequence: 1 TQHGIRLPLRSGLGGA 16

Scoring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Word size: 1

Total number of hits satisfying chosen parameters: 2397162

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US10726967/runat_26072005_130816_6503/app_query.fasta_1.199
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=olip2n.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10726967_@CGN_1_1_105_@runat_26072005_130816_6503 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	16	100.0	1287	3	US-09-548-372D-50	Sequence 50, Appl
2	16	100.0	1287	3	US-09-548-367D-50	Sequence 50, Appl
3	16	100.0	1287	4	US-09-551-853D-50	Sequence 50, Appl
4	16	100.0	1287	4	US-09-416-901B-50	Sequence 50, Appl
5	16	100.0	1287	4	US-09-548-376D-50	Sequence 50, Appl
6	16	100.0	1287	4	US-09-794-927A-50	Sequence 50, Appl
7	16	100.0	1287	4	US-09-548-373D-50	Sequence 50, Appl
8	16	100.0	1287	4	US-09-795-847B-50	Sequence 50, Appl
9	16	100.0	1287	4	US-09-869-414-50	Sequence 50, Appl
10	16	100.0	1287	4	US-09-548-366F-50	Sequence 50, Appl
11	16	100.0	1287	4	US-09-548-368D-50	Sequence 50, Appl
12	16	100.0	1287	4	US-09-794-925A-50	Sequence 50, Appl
13	16	100.0	1302	3	US-09-548-372D-25	Sequence 25, Appl
14	16	100.0	1302	3	US-09-548-367D-25	Sequence 25, Appl
15	16	100.0	1302	4	US-09-551-853D-25	Sequence 25, Appl
16	16	100.0	1302	4	US-09-416-901B-25	Sequence 25, Appl
17	16	100.0	1302	4	US-09-548-376D-25	Sequence 25, Appl
18	16	100.0	1302	4	US-09-794-927A-25	Sequence 25, Appl
19	16	100.0	1302	4	US-09-548-373D-25	Sequence 25, Appl
20	16	100.0	1302	4	US-09-795-847B-25	Sequence 25, Appl
21	16	100.0	1302	4	US-09-869-414-25	Sequence 25, Appl
22	16	100.0	1302	4	US-09-548-366F-25	Sequence 25, Appl
23	16	100.0	1302	4	US-09-548-368D-25	Sequence 25, Appl
24	16	100.0	1302	4	US-09-794-925A-25	Sequence 25, Appl
25	16	100.0	1302	4	US-09-806-194A-25	Sequence 25, Appl
26	16	100.0	1305	3	US-09-548-372D-52	Sequence 52, Appl
27	16	100.0	1305	3	US-09-548-367D-52	Sequence 52, Appl
28	16	100.0	1305	4	US-09-551-853D-52	Sequence 52, Appl
29	16	100.0	1305	4	US-09-416-901B-52	Sequence 52, Appl
30	16	100.0	1305	4	US-09-548-376D-52	Sequence 52, Appl
31	16	100.0	1305	4	US-09-794-927A-52	Sequence 52, Appl
32	16	100.0	1305	4	US-09-548-373D-52	Sequence 52, Appl
33	16	100.0	1305	4	US-09-795-847B-52	Sequence 52, Appl
34	16	100.0	1305	4	US-09-869-414-52	Sequence 52, Appl
35	16	100.0	1305	4	US-09-548-366F-52	Sequence 52, Appl
36	16	100.0	1305	4	US-09-548-368D-52	Sequence 52, Appl
37	16	100.0	1305	4	US-09-794-925A-52	Sequence 52, Appl
38	16	100.0	1341	3	US-09-548-372D-21	Sequence 21, Appl
39	16	100.0	1341	3	US-09-548-367D-21	Sequence 21, Appl
40	16	100.0	1341	4	US-09-551-853D-21	Sequence 21, Appl
41	16	100.0	1341	4	US-09-416-901B-21	Sequence 21, Appl
42	16	100.0	1341	4	US-09-548-376D-21	Sequence 21, Appl
43	16	100.0	1341	4	US-09-794-927A-21	Sequence 21, Appl
44	16	100.0	1341	4	US-09-548-373D-21	Sequence 21, Appl
45	16	100.0	1341	4	US-09-795-847B-21	Sequence 21, Appl

ALIGNMENTS

RESULT 1
US-09-548-372D-50
; Sequence 50, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280I
; CURRENT APPLICATION NUMBER: US/09/548,372D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 50
; LENGTH: 1287
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Hu-Asp2(b) delta TM
US-09-548-372D-50

Alignment Scores:

Pred. No.:	1.48e-06	Length:	1287
Score:	16.00	Matches:	16
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	3	Gaps:	0

US-10-726-967A-3 (1-16) x US-09-548-372D-50 (1-1287)

```
Qy          1 ThrGlnHisGlyIleArgLeuProLeuArgSerGlyLeuGlyGlyAla 16
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 ACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCC 111
```

RESULT 2
US-09-548-367D-50
; Sequence 50, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280H
; CURRENT APPLICATION NUMBER: US/09/548,367D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 50
; LENGTH: 1287
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Hu-Asp2(b) delta TM
US-09-548-367D-50

Alignment Scores:

Pred. No.:	1.48e-06	Length:	1287
Score:	16.00	Matches:	16
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	3	Gaps:	0

US-10-726-967A-3 (1-16) x US-09-548-367D-50 (1-1287)

```
Qy          1 ThrGlnHisGlyIleArgLeuProLeuArgSerGlyLeuGlyGlyAla 16
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 ACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCC 111
```

RESULT 3
US-09-551-853D-50
; Sequence 50, Application US/09551853D
; Patent No. 6500667
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280L
; CURRENT APPLICATION NUMBER: US/09/551,853D
; CURRENT FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 50
; LENGTH: 1287
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Hu-Asp2(b) delta TM
US-09-551-853D-50

Alignment Scores:

Pred. No.:	1.48e-06	Length:	1287
Score:	16.00	Matches:	16
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	4	Gaps:	0

US-10-726-967A-3 (1-16) x US-09-551-853D-50 (1-1287)

```
Qy          1 ThrGlnHisGlyIleArgLeuProLeuArgSerGlyLeuGlyGlyAla 16
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 ACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCC 111
```

RESULT 4
US-09-416-901B-50
; Sequence 50, Application US/09416901B
; Patent No. 6699671
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280A
; CURRENT APPLICATION NUMBER: US/09/416,901B
; CURRENT FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 50
; LENGTH: 1287
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Hu-Asp2(b) delta TM
US-09-416-901B-50

Alignment Scores:

Pred. No.:	1.48e-06	Length:	1287
Score:	16.00	Matches:	16
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	4	Gaps:	0

US-10-726-967A-3 (1-16) x US-09-416-901B-50 (1-1287)

```
Qy          1 ThrGlnHisGlyIleArgLeuProLeuArgSerGlyLeuGlyGlyAla 16
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 ACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCC 111
```

RESULT 5
US-09-548-376D-50
; Sequence 50, Application US/09548376D
; Patent No. 6706485
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR
; TITLE OF INVENTION: AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280F

; CURRENT APPLICATION NUMBER: US/09/548,376D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 50
; LENGTH: 1287
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Hu-Asp2(b) delta TM
US-09-548-376D-50

Alignment Scores:

Pred. No.:	1.48e-06	Length:	1287
Score:	16.00	Matches:	16
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	4	Gaps:	0

US-10-726-967A-3 (1-16) x US-09-548-376D-50 (1-1287)

```
Qy          1 ThrGlnHisGlyIleArgLeuProLeuArgSerGlyLeuGlyGlyAla 16
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 ACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCC 111
```

RESULT 6
US-09-794-927A-50
; Sequence 50, Application US/09794927A
; Patent No. 6727074
; GENERAL INFORMATION:
; APPLICANT: Gurney et al.
; TITLE OF INVENTION: Alzheimer's Disease Secretase, APP Substrates Therefor and Uses
; TITLE OF INVENTION: Therefor
; FILE REFERENCE: 29915/6280FG
; CURRENT APPLICATION NUMBER: US/09/794,927A
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 50
; LENGTH: 1287
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Hu-Asp2(b) delta TM
US-09-794-927A-50

Alignment Scores:

Pred. No.:	1.48e-06	Length:	1287
Score:	16.00	Matches:	16
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	4	Gaps:	0

US-10-726-967A-3 (1-16) x US-09-794-927A-50 (1-1287)

```
Qy          1 ThrGlnHisGlyIleArgLeuProLeuArgSerGlyLeuGlyGlyAla 16
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 ACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCC 111
```

RESULT 7
US-09-548-373D-50
; Sequence 50, Application US/09548373D
; Patent No. 6737510
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280B
; CURRENT APPLICATION NUMBER: US/09/548,373D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 50
; LENGTH: 1287
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Hu-Asp2(b) delta TM
US-09-548-373D-50

Alignment Scores:

Pred. No.:	1.48e-06	Length:	1287
Score:	16.00	Matches:	16
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	4	Gaps:	0

US-10-726-967A-3 (1-16) x US-09-548-373D-50 (1-1287)

```
Qy          1 ThrGlnHisGlyIleArgLeuProLeuArgSerGlyLeuGlyGlyAla 16
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 ACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCC 111
```

RESULT 8
US-09-795-847B-50
; Sequence 50, Application US/09795847B
; Patent No. 6753163
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280DE
; CURRENT APPLICATION NUMBER: US/09/795,847B
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594

```
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 74
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 50
;    LENGTH: 1287
;    TYPE: DNA
;    ORGANISM: Artificial sequence
;    FEATURE:
;    OTHER INFORMATION: Hu-Asp2(b) delta TM
US-09-795-847B-50

Alignment Scores:
Pred. No.:              1.48e-06        Length:         1287
Score:                  16.00           Matches:        16
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     4               Gaps:           0

US-10-726-967A-3 (1-16) x US-09-795-847B-50 (1-1287)

Qy          1 ThrGlnHisGlyIleArgLeuProLeuArgSerGlyLeuGlyGlyAla 16
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 ACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCC 111

RESULT 9
US-09-869-414-50
; Sequence 50, Application US/09869414
; Patent No. 6790610
; GENERAL INFORMATION:
;  APPLICANT: Beinkowski et al.
;  TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE: 28341/6280M
;  CURRENT APPLICATION NUMBER: US/09/869,414
;  CURRENT FILING DATE:  2001-06-27
;  PRIOR APPLICATION NUMBER: 09/416,901
;  PRIOR FILING DATE: 1999-10-13
;  PRIOR APPLICATION NUMBER: 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 50
;    LENGTH: 1287
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Description of Artificial Sequence: Hu-Asp2(b)
;    OTHER INFORMATION: delta TM
US-09-869-414-50

Alignment Scores:
Pred. No.:              1.48e-06        Length:         1287
Score:                  16.00           Matches:        16
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     4               Gaps:           0

US-10-726-967A-3 (1-16) x US-09-869-414-50 (1-1287)

Qy          1 ThrGlnHisGlyIleArgLeuProLeuArgSerGlyLeuGlyGlyAla 16
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 ACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCC 111

RESULT 10
US-09-548-366F-50
; Sequence 50, Application US/09548366F
; Patent No. 6797487
; GENERAL INFORMATION:
;  APPLICANT: GURNEY ET AL.
;  TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 29915/6280J
;  CURRENT APPLICATION NUMBER: US/09/548,366F
;  CURRENT FILING DATE:  2000-04-12
;  PRIOR APPLICATION NUMBER: US 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 50
;    LENGTH: 1287
;    TYPE: DNA
;    ORGANISM: Artificial sequence
;    FEATURE:
;    OTHER INFORMATION: Hu-Asp2(b) delta TM
US-09-548-366F-50

Alignment Scores:
Pred. No.:              1.48e-06        Length:         1287
Score:                  16.00           Matches:        16
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     4               Gaps:           0

US-10-726-967A-3 (1-16) x US-09-548-366F-50 (1-1287)

Qy          1 ThrGlnHisGlyIleArgLeuProLeuArgSerGlyLeuGlyGlyAla 16
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 ACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCC 111

RESULT 11
US-09-548-368D-50
; Sequence 50, Application US/09548368D
; Patent No. 6825023
; GENERAL INFORMATION:
;  APPLICANT: GURNEY ET AL.
;  TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 29915/6280C
;  CURRENT APPLICATION NUMBER: US/09/548,368D
;  CURRENT FILING DATE:  2000-04-12
;  PRIOR APPLICATION NUMBER: US 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 50
;    LENGTH: 1287
;    TYPE: DNA
;    ORGANISM: Artificial sequence
;    FEATURE:
;    OTHER INFORMATION: Hu-Asp2(b) delta TM
US-09-548-368D-50

Alignment Scores:
Pred. No.:              1.48e-06        Length:         1287
Score:                  16.00           Matches:        16
```

```
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
DB:                     4              Gaps:          0

US-10-726-967A-3 (1-16) x US-09-548-368D-50 (1-1287)

Qy          1 ThrGlnHisGlyIleArgLeuProLeuArgSerGlyLeuGlyGlyAla 16
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 ACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCC 111

RESULT 12
US-09-794-925A-50
; Sequence 50, Application US/09794925A
; Patent No. 6828117
; GENERAL INFORMATION:
;  APPLICANT: Gurney et al.
;  TITLE OF INVENTION: Alzheimer's Disease Secretase, APP Substrates Therefor and Uses
;  TITLE OF INVENTION:  Therefor
;  FILE REFERENCE: 29915/6280HI
;  CURRENT APPLICATION NUMBER: US/09/794,925A
;  CURRENT FILING DATE:  2001-02-27
;  PRIOR APPLICATION NUMBER: 09/416,901
;  PRIOR FILING DATE: 1999-10-13
;  PRIOR APPLICATION NUMBER: 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 74
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 50
;   LENGTH: 1287
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Hu-Asp2(b) delta TM
US-09-794-925A-50

Alignment Scores:
Pred. No.:              1.48e-06       Length:        1287
Score:                  16.00          Matches:       16
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
DB:                     4              Gaps:          0

US-10-726-967A-3 (1-16) x US-09-794-925A-50 (1-1287)

Qy          1 ThrGlnHisGlyIleArgLeuProLeuArgSerGlyLeuGlyGlyAla 16
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 ACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCC 111

RESULT 13
US-09-548-372D-25
; Sequence 25, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
;  APPLICANT: GURNEY ET AL.
;  TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 29915/6280I
;  CURRENT APPLICATION NUMBER: US/09/548,372D
;  CURRENT FILING DATE:  2000-04-12
;  PRIOR APPLICATION NUMBER: US 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
;   LENGTH: 1302
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-548-372D-25

Alignment Scores:
Pred. No.:              1.5e-06        Length:        1302
Score:                  16.00          Matches:       16
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
DB:                     3              Gaps:          0

US-10-726-967A-3 (1-16) x US-09-548-372D-25 (1-1302)

Qy          1 ThrGlnHisGlyIleArgLeuProLeuArgSerGlyLeuGlyGlyAla 16
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db          4 ACTCAGCATGGTATTCGTCTGCCACTGCGTAGCGGTCTGGGTGGTGCT 51

RESULT 14
US-09-548-367D-25
; Sequence 25, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
;  APPLICANT: GURNEY ET AL.
;  TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 29915/6280H
;  CURRENT APPLICATION NUMBER: US/09/548,367D
;  CURRENT FILING DATE:  2000-04-12
;  PRIOR APPLICATION NUMBER: US 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
;   LENGTH: 1302
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-548-367D-25

Alignment Scores:
Pred. No.:              1.5e-06        Length:        1302
Score:                  16.00          Matches:       16
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
DB:                     3              Gaps:          0

US-10-726-967A-3 (1-16) x US-09-548-367D-25 (1-1302)

Qy          1 ThrGlnHisGlyIleArgLeuProLeuArgSerGlyLeuGlyGlyAla 16
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db          4 ACTCAGCATGGTATTCGTCTGCCACTGCGTAGCGGTCTGGGTGGTGCT 51

RESULT 15
US-09-551-853D-25
; Sequence 25, Application US/09551853D
; Patent No. 6500667
; GENERAL INFORMATION:
;  APPLICANT: GURNEY ET AL.
;  TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
;  TITLE OF INVENTION:  THEREOF
```

; FILE REFERENCE: 29915/6280L
; CURRENT APPLICATION NUMBER: US/09/551,853D
; CURRENT FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 1302
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-551-853D-25

Alignment Scores:

Pred. No.:	1.5e-06	Length:	1302
Score:	16.00	Matches:	16
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	4	Gaps:	0

US-10-726-967A-3 (1-16) x US-09-551-853D-25 (1-1302)

```
Qy          1 ThrGlnHisGlyIleArgLeuProLeuArgSerGlyLeuGlyGlyAla 16
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db          4 ACTCAGCATGGTATTCGTCTGCCACTGCGTAGCGGTCTGGGTGGTGCT 51
```

Search completed: July 27, 2005, 20:38:13
Job time : 135 secs

GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: July 27, 2005, 19:03:29 ; Search time 625 Seconds
(without alignments)
165.537 Million cell updates/sec

Title: US-10-726-967A-3
Perfect score: 16
Sequence: 1 TQHGIRLPLRSGLGGA 16

Scoring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 7277826 seqs, 3233139505 residues

Word size: 1

Total number of hits satisfying chosen parameters: 14539411

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US10726967/runat_26072005_130817_6528/app_query.fasta_1.199
-DB=Published_Applications_NA -QFMT=fastap -SUFFIX=olip2n.rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1
-ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US10726967_@CGN_1_1_723_@runat_26072005_130817_6528
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
19: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq:*
20: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq:*
21: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq:*
22: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
23: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq:*
24: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
25: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	16	100.0	1287	9	US-09-794-927-50	Sequence 50, Appl
2	16	100.0	1287	9	US-09-795-847-50	Sequence 50, Appl
3	16	100.0	1287	9	US-09-794-743-50	Sequence 50, Appl
4	16	100.0	1287	9	US-09-794-748-50	Sequence 50, Appl
5	16	100.0	1287	9	US-09-794-925-50	Sequence 50, Appl
6	16	100.0	1287	9	US-09-681-442-50	Sequence 50, Appl
7	16	100.0	1287	10	US-09-869-414-50	Sequence 50, Appl
8	16	100.0	1287	10	US-09-548-366-50	Sequence 50, Appl
9	16	100.0	1287	18	US-10-652-927-50	Sequence 50, Appl
10	16	100.0	1287	18	US-10-652-830-50	Sequence 50, Appl
11	16	100.0	1287	19	US-10-652-045-50	Sequence 50, Appl
12	16	100.0	1287	20	US-10-476-935-50	Sequence 50, Appl
13	16	100.0	1287	21	US-10-477-076-50	Sequence 50, Appl
14	16	100.0	1302	9	US-09-794-927-25	Sequence 25, Appl
15	16	100.0	1302	9	US-09-795-847-25	Sequence 25, Appl
16	16	100.0	1302	9	US-09-794-743-25	Sequence 25, Appl
17	16	100.0	1302	9	US-09-794-748-25	Sequence 25, Appl
18	16	100.0	1302	9	US-09-794-925-25	Sequence 25, Appl
19	16	100.0	1302	9	US-09-681-442-25	Sequence 25, Appl
20	16	100.0	1302	10	US-09-869-414-25	Sequence 25, Appl
21	16	100.0	1302	10	US-09-548-366-25	Sequence 25, Appl
22	16	100.0	1302	18	US-10-652-927-25	Sequence 25, Appl
23	16	100.0	1302	18	US-10-652-830-25	Sequence 25, Appl
24	16	100.0	1302	19	US-10-652-045-25	Sequence 25, Appl
25	16	100.0	1302	20	US-10-476-935-25	Sequence 25, Appl
26	16	100.0	1302	21	US-10-940-867-25	Sequence 25, Appl
27	16	100.0	1302	21	US-10-477-076-25	Sequence 25, Appl
28	16	100.0	1305	9	US-09-794-927-52	Sequence 52, Appl
29	16	100.0	1305	9	US-09-795-847-52	Sequence 52, Appl
30	16	100.0	1305	9	US-09-794-743-52	Sequence 52, Appl
31	16	100.0	1305	9	US-09-794-748-52	Sequence 52, Appl
32	16	100.0	1305	9	US-09-794-925-52	Sequence 52, Appl
33	16	100.0	1305	9	US-09-681-442-52	Sequence 52, Appl
34	16	100.0	1305	10	US-09-869-414-52	Sequence 52, Appl
35	16	100.0	1305	10	US-09-548-366-52	Sequence 52, Appl
36	16	100.0	1305	18	US-10-652-927-52	Sequence 52, Appl
37	16	100.0	1305	18	US-10-652-830-52	Sequence 52, Appl
38	16	100.0	1305	19	US-10-652-045-52	Sequence 52, Appl
39	16	100.0	1305	20	US-10-476-935-52	Sequence 52, Appl
40	16	100.0	1305	21	US-10-477-076-52	Sequence 52, Appl
41	16	100.0	1341	9	US-09-794-927-21	Sequence 21, Appl
42	16	100.0	1341	9	US-09-795-847-21	Sequence 21, Appl
43	16	100.0	1341	9	US-09-794-743-21	Sequence 21, Appl
44	16	100.0	1341	9	US-09-794-748-21	Sequence 21, Appl
45	16	100.0	1341	9	US-09-794-925-21	Sequence 21, Appl

ALIGNMENTS

RESULT 1
US-09-794-927-50
; Sequence 50, Application US/09794927
; Patent No. US20010016324A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280FG
; CURRENT APPLICATION NUMBER: US/09/794,927
; CURRENT FILING DATE: 2001-02-27

; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 50
; LENGTH: 1287
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Hu-Asp2(b)
; OTHER INFORMATION: delta TM
US-09-794-927-50

Alignment Scores:

Pred. No.:	2.94e-06	Length:	1287
Score:	16.00	Matches:	16
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-10-726-967A-3 (1-16) x US-09-794-927-50 (1-1287)

```
Qy          1 ThrGlnHisGlyIleArgLeuProLeuArgSerGlyLeuGlyGlyAla 16
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 ACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCC 111
```

RESULT 2
US-09-795-847-50
; Sequence 50, Application US/09795847
; Patent No. US20010018208A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280DE
; CURRENT APPLICATION NUMBER: US/09/795,847
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 50
; LENGTH: 1287
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Hu-Asp2(b)
; OTHER INFORMATION: delta TM
US-09-795-847-50

Alignment Scores:

Pred. No.:	2.94e-06	Length:	1287
Score:	16.00	Matches:	16
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-10-726-967A-3 (1-16) x US-09-795-847-50 (1-1287)

```
Qy          1 ThrGlnHisGlyIleArgLeuProLeuArgSerGlyLeuGlyGlyAla 16
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 ACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCC 111
```

RESULT 3
US-09-794-743-50
; Sequence 50, Application US/09794743
; Patent No. US20010021391A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280BC
; CURRENT APPLICATION NUMBER: US/09/794,743
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 50
; LENGTH: 1287
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Hu-Asp2(b)
; OTHER INFORMATION: delta TM
US-09-794-743-50

Alignment Scores:

Pred. No.:	2.94e-06	Length:	1287
Score:	16.00	Matches:	16
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-10-726-967A-3 (1-16) x US-09-794-743-50 (1-1287)

```
Qy          1 ThrGlnHisGlyIleArgLeuProLeuArgSerGlyLeuGlyGlyAla 16
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 ACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCC 111
```

RESULT 4
US-09-794-748-50
; Sequence 50, Application US/09794748
; Patent No. US20020037315A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.

```
;  APPLICANT:  Yan, Riqiang
;  TITLE OF INVENTION:  ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
;  TITLE OF INVENTION:  USES
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE:  28341/6280JL
;  CURRENT APPLICATION NUMBER: US/09/794,748
;  CURRENT FILING DATE:  2001-02-27
;  PRIOR APPLICATION NUMBER:  09/416,901
;  PRIOR FILING DATE:  1999-10-13
;  PRIOR APPLICATION NUMBER:  60/155,493
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  09/404,133
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  PCT/US99/20881
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  60/101,594
;  PRIOR FILING DATE:  1998-09-24
;  NUMBER OF SEQ ID NOS:  73
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 50
;    LENGTH: 1287
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Description of Artificial Sequence: Hu-Asp2(b)
;    OTHER INFORMATION: delta TM
US-09-794-748-50

Alignment Scores:
Pred. No.:                2.94e-06        Length:         1287
Score:                    16.00           Matches:        16
Percent Similarity:       100.00%         Conservative:   0
Best Local Similarity:    100.00%         Mismatches:     0
Query Match:              100.00%         Indels:         0
DB:                       9               Gaps:           0

US-10-726-967A-3 (1-16) x US-09-794-748-50 (1-1287)

Qy          1 ThrGlnHisGlyIleArgLeuProLeuArgSerGlyLeuGlyGlyAla 16
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 ACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCC 111

RESULT 5
US-09-794-925-50
; Sequence 50, Application US/09794925
; Patent No. US20020064819A1
; GENERAL INFORMATION:
;  APPLICANT:  Gurney, Mark E.
;  APPLICANT:  Bienkowski, Michael J.
;  APPLICANT:  Heinrikson, Robert L.
;  APPLICANT:  Parodi, Luis A.
;  APPLICANT:  Yan, Riqiang
;  TITLE OF INVENTION:  ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE:  28341/6280HI
;  CURRENT APPLICATION NUMBER: US/09/794,925
;  CURRENT FILING DATE:  2001-02-27
;  PRIOR APPLICATION NUMBER:  09/416,901
;  PRIOR FILING DATE:  1999-10-13
;  PRIOR APPLICATION NUMBER:  60/155,493
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  09/404,133
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  PCT/US99/20881
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  60/101,594
;  PRIOR FILING DATE:  1998-09-24
;  NUMBER OF SEQ ID NOS:  73
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 50
;    LENGTH: 1287
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Description of Artificial Sequence: Hu-Asp2(b)
;    OTHER INFORMATION: delta TM
US-09-794-925-50

Alignment Scores:
Pred. No.:                2.94e-06        Length:         1287
Score:                    16.00           Matches:        16
Percent Similarity:       100.00%         Conservative:   0
Best Local Similarity:    100.00%         Mismatches:     0
Query Match:              100.00%         Indels:         0
DB:                       9               Gaps:           0

US-10-726-967A-3 (1-16) x US-09-794-925-50 (1-1287)

Qy          1 ThrGlnHisGlyIleArgLeuProLeuArgSerGlyLeuGlyGlyAla 16
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 ACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCC 111

RESULT 6
US-09-681-442-50
; Sequence 50, Application US/09681442
; Patent No. US20020081634A1
; GENERAL INFORMATION:
;  APPLICANT: Gurney, Mark E.
;  APPLICANT:  Bienkowski, Michael J.
;  APPLICANT:  Heinrikson, Robert L.
;  APPLICANT:  Parodi, Luis A.
;  APPLICANT:  Yan, Riqiang
;  TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE: 28341/6280FG
;  CURRENT APPLICATION NUMBER: US/09/681,442
;  CURRENT FILING DATE:  2001-04-05
;  PRIOR APPLICATION NUMBER: 09/416,901
;  PRIOR FILING DATE: 1999-10-13
;  PRIOR APPLICATION NUMBER: 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 50
;    LENGTH: 1287
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Description of Artificial Sequence: Hu-Asp2(b)
;    OTHER INFORMATION: delta TM
US-09-681-442-50

Alignment Scores:
Pred. No.:                2.94e-06        Length:         1287
Score:                    16.00           Matches:        16
Percent Similarity:       100.00%         Conservative:   0
Best Local Similarity:    100.00%         Mismatches:     0
Query Match:              100.00%         Indels:         0
DB:                       9               Gaps:           0

US-10-726-967A-3 (1-16) x US-09-681-442-50 (1-1287)

Qy          1 ThrGlnHisGlyIleArgLeuProLeuArgSerGlyLeuGlyGlyAla 16
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 ACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCC 111

RESULT 7
US-09-869-414-50
; Sequence 50, Application US/09869414
; Publication No. US20030077226A1
```

```
; GENERAL INFORMATION:
;  APPLICANT: Beinkowski et al.
;  TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE: 28341/6280M
;  CURRENT APPLICATION NUMBER: US/09/869,414
;  CURRENT FILING DATE:  2001-06-27
;  PRIOR APPLICATION NUMBER: 09/416,901
;  PRIOR FILING DATE: 1999-10-13
;  PRIOR APPLICATION NUMBER: 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 50
;   LENGTH: 1287
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Hu-Asp2(b)
;   OTHER INFORMATION: delta TM
US-09-869-414-50

Alignment Scores:
Pred. No.:              2.94e-06      Length:         1287
Score:                  16.00         Matches:        16
Percent Similarity:     100.00%       Conservative:   0
Best Local Similarity:  100.00%       Mismatches:     0
Query Match:            100.00%       Indels:         0
DB:                     10            Gaps:           0

US-10-726-967A-3 (1-16) x US-09-869-414-50 (1-1287)

Qy          1 ThrGlnHisGlyIleArgLeuProLeuArgSerGlyLeuGlyGlyAla 16
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 ACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCC 111

RESULT 8
US-09-548-366-50
; Sequence 50, Application US/09548366
; Publication No. US20030104365A1
; GENERAL INFORMATION:
;  APPLICANT:  Gurney, Mark E.
;  APPLICANT:  Bienkowski, Michael J.
;  APPLICANT:  Heinrikson, Robert L.
;  APPLICANT:  Parodi, Luis A.
;  APPLICANT:  Yan, Riqiang
;  TITLE OF INVENTION:  ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
;  TITLE OF INVENTION:  USES THEREFOR
;  FILE REFERENCE:  28341/6280A
;  CURRENT APPLICATION NUMBER: US/09/548,366
;  CURRENT FILING DATE:  2000-04-12
;  PRIOR APPLICATION NUMBER:  60/155,493
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  09/404,133
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  PCT/US99/20881
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  60/101,594
;  PRIOR FILING DATE:  1998-09-24
;  NUMBER OF SEQ ID NOS:  65
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 50
;   LENGTH: 1287
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Hu-Asp2(b)
;   OTHER INFORMATION: delta TM
US-09-548-366-50

Alignment Scores:
Pred. No.:              2.94e-06      Length:         1287
Score:                  16.00         Matches:        16
Percent Similarity:     100.00%       Conservative:   0
Best Local Similarity:  100.00%       Mismatches:     0
Query Match:            100.00%       Indels:         0
DB:                     10            Gaps:           0

US-10-726-967A-3 (1-16) x US-09-548-366-50 (1-1287)

Qy          1 ThrGlnHisGlyIleArgLeuProLeuArgSerGlyLeuGlyGlyAla 16
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 ACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCC 111

RESULT 9
US-10-652-927-50
; Sequence 50, Application US/10652927
; Publication No. US20040043408A1
; GENERAL INFORMATION:
;  APPLICANT: Gurney et al.
;  TITLE OF INVENTION: Alzheimer's Disease Secretase, APP Substrates Therefor and Uses
;  TITLE OF INVENTION:  Therefor
;  FILE REFERENCE: 29915/6280N3
;  CURRENT APPLICATION NUMBER: US/10/652,927
;  CURRENT FILING DATE:  2003-08-29
;  PRIOR APPLICATION NUMBER: 09/794,925
;  PRIOR FILING DATE: 2001-02-27
;  PRIOR APPLICATION NUMBER: 09/416,901
;  PRIOR FILING DATE: 1999-10-13
;  PRIOR APPLICATION NUMBER: 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 74
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 50
;   LENGTH: 1287
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Hu-Asp2(b) delta TM
US-10-652-927-50

Alignment Scores:
Pred. No.:              2.94e-06      Length:         1287
Score:                  16.00         Matches:        16
Percent Similarity:     100.00%       Conservative:   0
Best Local Similarity:  100.00%       Mismatches:     0
Query Match:            100.00%       Indels:         0
DB:                     18            Gaps:           0

US-10-726-967A-3 (1-16) x US-10-652-927-50 (1-1287)

Qy          1 ThrGlnHisGlyIleArgLeuProLeuArgSerGlyLeuGlyGlyAla 16
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 ACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCC 111

RESULT 10
US-10-652-830-50
; Sequence 50, Application US/10652830
; Publication No. US20040048303A1
; GENERAL INFORMATION:
;  APPLICANT: Gurney et al.
;  TITLE OF INVENTION: Alzheimer's Disease Secretase, APP Substrates Therefor and Uses
;  TITLE OF INVENTION:  Therefor
;  FILE REFERENCE: 29915/6280N1
```

```
;  CURRENT APPLICATION NUMBER: US/10/652,830
;  CURRENT FILING DATE:  2003-08-29
;  PRIOR APPLICATION NUMBER: 09/794,925
;  PRIOR FILING DATE: 2001-02-27
;  PRIOR APPLICATION NUMBER: 09/416,901
;  PRIOR FILING DATE: 1999-10-13
;  PRIOR APPLICATION NUMBER: 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 74
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 50
;    LENGTH: 1287
;    TYPE: DNA
;    ORGANISM: Artificial sequence
;    FEATURE:
;    OTHER INFORMATION: Hu-Asp2(b) delta TM
US-10-652-830-50

Alignment Scores:
Pred. No.:              2.94e-06        Length:         1287
Score:                  16.00           Matches:        16
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     18              Gaps:           0

US-10-726-967A-3 (1-16) x US-10-652-830-50 (1-1287)

Qy          1 ThrGlnHisGlyIleArgLeuProLeuArgSerGlyLeuGlyGlyAla 16
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 ACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCC 111

RESULT 11
US-10-652-045-50
; Sequence 50, Application US/10652045
; Publication No. US20040166507A1
; GENERAL INFORMATION:
;  APPLICANT: Gurney et al.
;  TITLE OF INVENTION: Alzheimer's Disease Secretase, APP Substrates Therefor and Uses
;  TITLE OF INVENTION:  Therefor
;  FILE REFERENCE: 29915/6280N2
;  CURRENT APPLICATION NUMBER: US/10/652,045
;  CURRENT FILING DATE:  2003-08-29
;  PRIOR APPLICATION NUMBER: 09/794,925
;  PRIOR FILING DATE: 2001-02-27
;  PRIOR APPLICATION NUMBER: 09/416,901
;  PRIOR FILING DATE: 1999-10-13
;  PRIOR APPLICATION NUMBER: 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 74
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 50
;    LENGTH: 1287
;    TYPE: DNA
;    ORGANISM: Artificial sequence
;    FEATURE:
;    OTHER INFORMATION: Hu-Asp2(b) delta TM
US-10-652-045-50

Alignment Scores:
Pred. No.:              2.94e-06        Length:         1287
Score:                  16.00           Matches:        16
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     19              Gaps:           0

US-10-726-967A-3 (1-16) x US-10-652-045-50 (1-1287)

Qy          1 ThrGlnHisGlyIleArgLeuProLeuArgSerGlyLeuGlyGlyAla 16
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 ACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCC 111

RESULT 12
US-10-476-935-50
; Sequence 50, Application US/10476935
; Publication No. US20040234976A1
; GENERAL INFORMATION:
;  APPLICANT: Beinkowski et al.
;  TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE: 28341/6280M1
;  CURRENT APPLICATION NUMBER: US/10/476,935
;  CURRENT FILING DATE:  2003-11-06
;  PRIOR APPLICATION NUMBER: 09/416,901
;  PRIOR FILING DATE: 1999-10-13
;  PRIOR APPLICATION NUMBER: 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 50
;    LENGTH: 1287
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Description of Artificial Sequence: Hu-Asp2(b)
;    OTHER INFORMATION: delta TM
US-10-476-935-50

Alignment Scores:
Pred. No.:              2.94e-06        Length:         1287
Score:                  16.00           Matches:        16
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     20              Gaps:           0

US-10-726-967A-3 (1-16) x US-10-476-935-50 (1-1287)

Qy          1 ThrGlnHisGlyIleArgLeuProLeuArgSerGlyLeuGlyGlyAla 16
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 ACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCC 111

RESULT 13
US-10-477-076-50
; Sequence 50, Application US/10477076
; Publication No. US20050080232A1
; GENERAL INFORMATION:
;  APPLICANT: Beinkowski et al.
;  TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE: 28341/6280M2
;  CURRENT APPLICATION NUMBER: US/10/477,076
;  CURRENT FILING DATE:  2003-11-06
;  PRIOR APPLICATION NUMBER: 09/416,901
;  PRIOR FILING DATE: 1999-10-13
;  PRIOR APPLICATION NUMBER: 60/155,493
;  PRIOR FILING DATE: 1999-09-23
```

```
;  PRIOR APPLICATION NUMBER: 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 50
;   LENGTH: 1287
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Hu-Asp2(b)
;   OTHER INFORMATION: delta TM
US-10-477-076-50

Alignment Scores:
Pred. No.:              2.94e-06      Length:         1287
Score:                  16.00         Matches:        16
Percent Similarity:     100.00%       Conservative:   0
Best Local Similarity:  100.00%       Mismatches:     0
Query Match:            100.00%       Indels:         0
DB:                     21            Gaps:           0

US-10-726-967A-3 (1-16) x US-10-477-076-50 (1-1287)

Qy          1 ThrGlnHisGlyIleArgLeuProLeuArgSerGlyLeuGlyGlyAla 16
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 ACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCC 111

RESULT 14
US-09-794-927-25
; Sequence 25, Application US/09794927
; Patent No. US20010016324A1
; GENERAL INFORMATION:
;  APPLICANT:  Gurney, Mark E.
;  APPLICANT:  Bienkowski, Michael J.
;  APPLICANT:  Heinrikson, Robert L.
;  APPLICANT:  Parodi, Luis A.
;  APPLICANT:  Yan, Riqiang
;  TITLE OF INVENTION:  ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
;  TITLE OF INVENTION:  USES
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE:  28341/6280FG
;  CURRENT APPLICATION NUMBER: US/09/794,927
;  CURRENT FILING DATE:  2001-02-27
;  PRIOR APPLICATION NUMBER:  09/416,901
;  PRIOR FILING DATE:  1999-10-13
;  PRIOR APPLICATION NUMBER:  60/155,493
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  09/404,133
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  PCT/US99/20881
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  60/101,594
;  PRIOR FILING DATE:  1998-09-24
;  NUMBER OF SEQ ID NOS:  73
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 25
;   LENGTH: 1302
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-794-927-25

Alignment Scores:
Pred. No.:              2.97e-06      Length:         1302
Score:                  16.00         Matches:        16
Percent Similarity:     100.00%       Conservative:   0
Best Local Similarity:  100.00%       Mismatches:     0
Query Match:            100.00%       Indels:         0
DB:                     9             Gaps:           0

US-10-726-967A-3 (1-16) x US-09-794-927-25 (1-1302)

Qy          1 ThrGlnHisGlyIleArgLeuProLeuArgSerGlyLeuGlyGlyAla 16
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db          4 ACTCAGCATGGTATTCGTCTGCCACTGCGTAGCGGTCTGGGTGGTGCT 51

RESULT 15
US-09-795-847-25
; Sequence 25, Application US/09795847
; Patent No. US20010018208A1
; GENERAL INFORMATION:
;  APPLICANT:  Gurney, Mark E.
;  APPLICANT:  Bienkowski, Michael J.
;  APPLICANT:  Heinrikson, Robert L.
;  APPLICANT:  Parodi, Luis A.
;  APPLICANT:  Yan, Riqiang
;  TITLE OF INVENTION:  ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
;  TITLE OF INVENTION:  USES
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE:  28341/6280DE
;  CURRENT APPLICATION NUMBER: US/09/795,847
;  CURRENT FILING DATE:  2001-02-28
;  PRIOR APPLICATION NUMBER:  09/416,901
;  PRIOR FILING DATE:  1999-10-13
;  PRIOR APPLICATION NUMBER:  60/155,493
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  09/404,133
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  PCT/US99/20881
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  60/101,594
;  PRIOR FILING DATE:  1998-09-24
;  NUMBER OF SEQ ID NOS:  73
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 25
;   LENGTH: 1302
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-795-847-25

Alignment Scores:
Pred. No.:              2.97e-06      Length:         1302
Score:                  16.00         Matches:        16
Percent Similarity:     100.00%       Conservative:   0
Best Local Similarity:  100.00%       Mismatches:     0
Query Match:            100.00%       Indels:         0
DB:                     9             Gaps:           0

US-10-726-967A-3 (1-16) x US-09-795-847-25 (1-1302)

Qy          1 ThrGlnHisGlyIleArgLeuProLeuArgSerGlyLeuGlyGlyAla 16
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db          4 ACTCAGCATGGTATTCGTCTGCCACTGCGTAGCGGTCTGGGTGGTGCT 51


Search completed: July 27, 2005, 20:48:51
Job time : 626 secs
```

GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: July 27, 2005, 18:50:24 ; Search time 3143 Seconds
(without alignments)
193.773 Million cell updates/sec

Title: US-10-726-967A-3
Perfect score: 16
Sequence: 1 TQHGIRLPLRSGLGGA 16

Scoring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Word size: 1

Total number of hits satisfying chosen parameters: 68473592

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US10726967/runat_26072005_130816_6487/app_query.fasta_1.199
-DB=EST -QFMT=fastap -SUFFIX=olip2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10726967_@CGN_1_1_5180_@runat_26072005_130816_6487 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	16	100.0	611	7	CN484125	CN484125 hw42d08.y
	2	16	100.0	1506	9	AY417360	AY417360 Homo sapi
	3	13	81.2	424	4	BI337739	BI337739 361259 MA
	4	13	81.2	563	4	BG833894	BG833894 351953 MA
	5	13	81.2	616	5	BP452814	BP452814 BP452814
c	6	11	68.8	171	9	CE200035	CE200035 tigr-gss-
	7	10	62.5	493	7	CN692524	CN692524 E0324B10-
	8	10	62.5	533	7	CN697484	CN697484 E0394H10-
	9	10	62.5	547	7	CF903755	CF903755 A0413D10-
	10	10	62.5	563	7	CF906581	CF906581 A0448H07-
	11	10	62.5	576	7	CF171218	CF171218 B0839F04-
	12	10	62.5	600	6	BY713879	BY713879 BY713879
	13	10	62.5	619	2	BB644736	BB644736 BB644736
	14	10	62.5	637	6	CD348605	CD348605 UI-M-FY0-
	15	10	62.5	639	2	BB632244	BB632244 BB632244
	16	10	62.5	639	2	BB652612	BB652612 BB652612
	17	10	62.5	640	6	BY724111	BY724111 BY724111
	18	10	62.5	650	2	BB624169	BB624169 BB624169
	19	10	62.5	653	6	BY727440	BY727440 BY727440
	20	10	62.5	673	2	BB640442	BB640442 BB640442
	21	10	62.5	673	2	BB650860	BB650860 BB650860
	22	10	62.5	727	6	CA749486	CA749486 UI-M-FY0-
	23	10	62.5	836	5	BX374914	BX374914 BX374914
	24	10	62.5	844	1	AL544727	AL544727 AL544727
	25	10	62.5	1123	5	BX376891	BX376891 BX376891
	26	10	62.5	1506	9	AY417362	AY417362 Mus muscu
	27	10	62.5	3634	3	AK041285	AK041285 Mus muscu
	28	10	62.5	3859	3	AK014464	AK014464 Mus muscu
	29	10	62.5	3877	3	AK033112	AK033112 Mus muscu
	30	10	62.5	4046	3	AK049626	AK049626 Mus muscu
	31	10	62.5	4048	3	AK082317	AK082317 Mus muscu
	32	10	62.5	4101	3	AK046175	AK046175 Mus muscu
	33	9	56.2	409	6	CB215573	CB215573 NISC_np07
	34	9	56.2	566	8	BH881298	BH881298 hv24E08.b
c	35	9	56.2	727	9	CG324082	CG324082 OG0BA83TV
	36	9	56.2	913	9	CG310449	CG310449 OGWAH26TV
	37	9	56.2	986	5	BX393934	BX393934 BX393934
c	38	9	56.2	1765	2	BF572300	BF572300 602077748
	39	8	50.0	156	7	CO060378	CO060378 est_k_bre
c	40	8	50.0	220	7	CF681698	CF681698 CCAAO96TR
	41	8	50.0	234	2	BB569323	BB569323 BB569323
c	42	8	50.0	258	2	BF872950	BF872950 CM0-ET012
	43	8	50.0	272	4	BM258402	BM258402 523194 MA
	44	8	50.0	295	4	BM574145	BM574145 fx59f10.y
	45	8	50.0	305	9	CC810341	CC810341 ZMMBBc047

ALIGNMENTS

RESULT 1
CN484125
LOCUS CN484125 611 bp mRNA linear EST 26-APR-2004
DEFINITION hw42d08.y2 Human primary human ocular pericytes. Unamplified (hw)
Homo sapiens cDNA clone hw42d08 5', mRNA sequence.
ACCESSION CN484125
VERSION CN484125.1 GI:46565629
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 611)
AUTHORS Tsai,J.Y. and Wistow,G.
TITLE Expressed sequence tag analysis of cultured primary human ocular pericytes
JOURNAL Unpublished (2004)
COMMENT Contact: Wistow G
Section on Molecular Structure and Function
National Eye Institute
6/331, NIH, Bethesda, MD 20892-2740, USA
Tel: 301 402 3452
Fax: 301 496 0078
Email: graeme@helix.nih.gov
Plate: 42 row: d column: 08
Seq primer: M13RP1 reverse primer (ABI).
FEATURES Location/Qualifiers
source 1. .611
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="hw42d08"
/cell_type="pericytes"

/dev_stage="Adult"
/lab_host="EMDH10B"
/clone_lib="Human primary human ocular pericytes. Unamplified (hw)"
/note="Organ: Eye; Vector: pSport1; RNA was extracted from primary human pericytes in culture. A directionally cloned cDNA library in the pSPORT1 vector (Invitrogen) was constructed at Bioserve Biotechnology (Laurel MD) essentially following the protocols of the SuperScript Plasmid System full details of which are contained in the manufacturer's Instruction manual (http://www.lifetech.com/). First strand synthesis was carried out using a Not I primer-adapter [5'-pGACTAGTTCTAGATCGCGAGCGGCCGCCC(T)15-3']. cDNA was cloned in Not I/Sal I sites. EST analysis was performed at the NIH Intramural Sequencing Center (NISC)."

ORIGIN

Alignment Scores:

Pred. No.:	9.47e-06	Length:	611
Score:	16.00	Matches:	16
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	7	Gaps:	0

US-10-726-967A-3 (1-16) x CN484125 (1-611)

```
Qy          1 ThrGlnHisGlyIleArgLeuProLeuArgSerGlyLeuGlyGlyAla 16
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 ACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCC 428
```

RESULT 2
AY417360
LOCUS AY417360 1506 bp DNA linear GSS 17-DEC-2003
DEFINITION Homo sapiens BACE gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
ACCESSION AY417360
VERSION AY417360.1 GI:39773320
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1506)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1506)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.
FEATURES Location/Qualifiers
source 1. .1506
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
gene <1. .>1506
/gene="BACE"
/locus_tag="HCM6198"
ORIGIN

Alignment Scores:

Pred. No.:	2.11e-05	Length:	1506
Score:	16.00	Matches:	16
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-10-726-967A-3 (1-16) x AY417360 (1-1506)

```
Qy          1 ThrGlnHisGlyIleArgLeuProLeuArgSerGlyLeuGlyGlyAla 16
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 ACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCC 111
```

RESULT 3
BI337739
LOCUS BI337739 424 bp mRNA linear EST 30-JUL-2001
DEFINITION 361259 MARC 1PIG Sus scrofa cDNA 5', mRNA sequence.
ACCESSION BI337739
VERSION BI337739.1 GI:15031022
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 424)
AUTHORS Fahrenkrug,S.C., Smith,T.P.L., Freking,B.A., Cho,J., White,J., Vallet,J., Wise,T., Rohrer,G.A., Pertea,G., Sultana,R., Quackenbush,J. and Keele,J.W.
TITLE Porcine gene discovery by normalized cDNA-library sequencing and EST cluster assembly
JOURNAL Mamm. Genome 13 (8), 475-478 (2002)
MEDLINE 22213789
PUBMED 12226715
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.
PCR PRimers
FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
Plate: 126 row: K column: 16
Seq primer: ATTTAGGTGACACTATAG.
FEATURES Location/Qualifiers
source 1. .424
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 1PIG"
/note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI; Library made from pooled tissue from day 11, 13, 15, 20, and 30 embryos."
ORIGIN

Alignment Scores:

Pred. No.:	0.00572	Length:	424
Score:	13.00	Matches:	13
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	81.25%	Indels:	0
DB:	4	Gaps:	0

US-10-726-967A-3 (1-16) x BI337739 (1-424)

```
Qy          4 GlyIleArgLeuProLeuArgSerGlyLeuGlyGlyAla 16
              |||||||||||||||||||||||||||||||||||||||
```

```
Db        376 GGCATCCGGCTGCCCCTGCGAAGCGGCCTTGGGGGGGCA 414

RESULT 4
BG833894
LOCUS       BG833894                563 bp    mRNA    linear   EST 25-MAY-2001
DEFINITION  351953 MARC 1PIG Sus scrofa cDNA 5', mRNA sequence.
ACCESSION   BG833894
VERSION     BG833894.1  GI:14198715
KEYWORDS    EST.
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to 563)
  AUTHORS   Fahrenkrug,S.C., Smith,T.P.L., Freking,B.A., Cho,J., White,J.,
            Vallet,J., Wise,T., Rohrer,G.A., Pertea,G., Sultana,R.,
            Quackenbush,J. and Keele,J.W.
  TITLE     Porcine gene discovery by normalized cDNA-library sequencing and
            EST cluster assembly
  JOURNAL   Mamm. Genome 13 (8), 475-478 (2002)
  MEDLINE   22213789
   PUBMED   12226715
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called and alt_trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -minscore 18
            and -minmatch 12 options.
            PCR PRimers
            FORWARD: AGGAAACAGCTATGACCAT
            BACKWARD: GTTTTCCCAGTCACGACG
            Plate: 111  row: G  column: 20
            Seq primer: ATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source          1. .563
                     /organism="Sus scrofa"
                     /mol_type="mRNA"
                     /db_xref="taxon:9823"
                     /tissue_type="pooled"
                     /lab_host="DH10B"
                     /clone_lib="MARC 1PIG"
                     /note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
                     Library made from pooled tissue from day 11, 13, 15, 20,
                     and 30 embryos."
ORIGIN

Alignment Scores:
Pred. No.:                0.00737        Length:          563
Score:                    13.00          Matches:         13
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              81.25%         Indels:          0
DB:                       4              Gaps:            0

US-10-726-967A-3 (1-16) x BG833894 (1-563)

Qy          4 GlyIleArgLeuProLeuArgSerGlyLeuGlyGlyAla 16
              ||||||||||||||||||||||||||||||||||||||||
Db        504 GGCATCCGGCTACCCCTGCGAAGCGGCCTTGGGGGGGCA 542

RESULT 5
BP452814
LOCUS       BP452814                616 bp    mRNA    linear   EST 30-DEC-2003
DEFINITION  BP452814 full-length enriched swine cDNA library, adult liver Sus
            scrofa cDNA clone LVRM10122F10 5', mRNA sequence.
ACCESSION   BP452814
VERSION     BP452814.1  GI:40442881
KEYWORDS    EST.
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to 616)
  AUTHORS   Uenishi,H., Eguchi,T., Suzuki,K., Sawazaki,T., Toki,D., Shinkai,H.,
            Okumura,N., Hamasima,N. and Awata,T.
  TITLE     PEDE (Pig EST Data Explorer): construction of a database for ESTs
            derived from porcine full-length cDNA libraries
  JOURNAL   Nucleic Acids Res. 32 (1), D484-D488 (2004)
COMMENT     Contact: Hirohide Uenishi
            Animal Genome Laboratory, Genome Research Department
            National Institute of Agrobiological Sciences
            2 Ikenodai, Tsukuba, Ibaraki 305-8602, Japan
            Tel: +81-29-838-8627
            Fax: +81-29-838-8627
            Email: huenishi@affrc.go.jp
            EST project with full-length enriched cDNA libraries carried out in
            Animal Genome Research Program (Japan) by National Institute of
            Agrobiological Sciences and STAFF-Institute
            Single pass sequencing of clones derived from oligo-capped cDNA
            library
            Vector sequences were eliminated by RepeatMasker version 2002/07/13
            and crossmatch version 0.990319
            Low quality bases were trimmed based on the quality values.
FEATURES             Location/Qualifiers
     source          1. .616
                     /organism="Sus scrofa"
                     /mol_type="mRNA"
                     /db_xref="taxon:9823"
                     /clone="LVRM10122F10"
                     /tissue_type="liver"
                     /dev_stage="adult"
                     /clone_lib="full-length enriched swine cDNA library, adult
                     liver"
ORIGIN

Alignment Scores:
Pred. No.:                0.00798        Length:          616
Score:                    13.00          Matches:         13
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              81.25%         Indels:          0
DB:                       5              Gaps:            0

US-10-726-967A-3 (1-16) x BP452814 (1-616)

Qy          4 GlyIleArgLeuProLeuArgSerGlyLeuGlyGlyAla 16
              ||||||||||||||||||||||||||||||||||||||||
Db        548 GGCATCCGGCTACCCCTGCGAAGCGGCCTTGGGGGGGCA 586

RESULT 6
CE200035/c
LOCUS       CE200035                171 bp    DNA     linear   GSS 25-SEP-2003
DEFINITION  tigr-gss-dog-17000372217391 Dog Library Canis familiaris genomic,
            genomic survey sequence.
ACCESSION   CE200035
VERSION     CE200035.1  GI:35355688
KEYWORDS    GSS.
SOURCE      Canis familiaris (dog)
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE   1  (bases 1 to 171)
  AUTHORS   Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
            Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
            Venter,J.C.
  TITLE     The dog genome: survey sequencing and comparative analysis
  JOURNAL   Science 301 (5641), 1898-1903 (2003)
  MEDLINE   22875432
   PUBMED   14512627
COMMENT     Contact: Kirkness EF
            The Institute for Genomic Research
            Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
            Rockville, MD 20850, USA
```

```
            Tel: 301-838-0200
            Fax: 301-838-0208
            Email: ekirknes@tigr.org
            Class: shotgun.
FEATURES              Location/Qualifiers
     source           1. .171
                      /organism="Canis familiaris"
                      /mol_type="genomic DNA"
                      /strain="Standard Poodle"
                      /db_xref="taxon:9615"
                      /clone_lib="Dog Library"
                      /note="Site_1: BstXI; Libraries were prepared from
                      peripheral blood"
ORIGIN

Alignment Scores:
Pred. No.:                0.227          Length:          171
Score:                    11.00          Matches:         11
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              68.75%         Indels:          0
DB:                       9              Gaps:            0

US-10-726-967A-3 (1-16) x CE200035 (1-171)

Qy          4 GlyIleArgLeuProLeuArgSerGlyLeuGly 14
              ||||||||||||||||||||||||||||||||
Db        168 GGCATCCGGCTGCCCCTGCGCAGCGGGCTGGGG 136

RESULT 7
CN692524
LOCUS       CN692524                 493 bp    mRNA    linear   EST 18-MAY-2004
DEFINITION  E0324B10-5 NIA Mouse E10.5 whole embryo cDNA library (Long) Mus
            musculus cDNA clone NIA:E0324B10 IMAGE:30861237 5', mRNA sequence.
ACCESSION   CN692524
VERSION     CN692524.1  GI:47461272
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 493)
  AUTHORS   Sharov,A.A., Piao,Y., Matoba,R., Dudekula,D.B., Qian,Y.,
            VanBuren,V., Falco,G., Martin,P.R., Stagg,C.A., Bassey,U.C.,
            Wang,Y., Carter,M.G., Hamatani,T., Aiba,K., Akutsu,H., Sharova,L.,
            Tanaka,T.S., Kimber,W.L., Yoshikawa,T., Jaradat,S.A., Pantano,S.,
            Nagaraja,R., Boheler,K.R., Taub,D., Hodes,R.J., Longo,D.L.,
            Schlessinger,D., Keller,J., Klotz,E., Kelsoe,G., Umezawa,A.,
            Vescovi,A.L., Rossant,J., Kunath,T., Hogan,B.L., Curci,A.,
            D'Urso,M., Kelso,J., Hide,W. and Ko,M.S.
  TITLE     Transcriptome analysis of mouse stem cells and early embryos
  JOURNAL   PLoS Biol. 1 (3), 410-419 (2003)
COMMENT     Contact: Dawood B. Dudekula
            Laboratory of Genetics
            National Institute on Aging/National Institutes of Health
            333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
            Email: cdna@lgsun.grc.nia.nih.gov
            Plate: E0324  row: B  column: 10
            Seq primer: M13 Reverse
            High quality sequence stop: 493
            POLYA=No.
FEATURES              Location/Qualifiers
     source           1. .493
                      /organism="Mus musculus"
                      /mol_type="mRNA"
                      /strain="C57BL/6J"
                      /db_xref="niaEST:E0324B10-5"
                      /db_xref="taxon:10090"
                      /clone="NIA:E0324B10 IMAGE:30861237"
                      /tissue_type="whole embryo including extraembryonic
                      tissues at 10.5-days postcoitum"
                      /dev_stage="E10.5"
                      /lab_host="DH10B"
                      /clone_lib="NIA Mouse E10.5 whole embryo cDNA library
                      (Long)"
                      /note="Vector: pCMV-SPORT6 (Invitrogen); Site_1: SalI;
                      Site_2: NotI; Mouse cDNA project by the Laboratory of
                      Genetics, National Institute on Aging (NIA), Intramural
                      Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA).
                      This is a long-transcript enriched cDNA library (Ref.
                      Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total
                      RNAs were extracted from a pool of 8 embryos at 10.5-days
                      postcoitum. Double-stranded cDNAs were synthesized with an
                      Oligo(dT) primer [Invitrogen:
                      5'-pGACTAGTTCTAGATCGCGAGCGGCCGCCCTTTTTTTTTTTTTT-3'] from
                      2ug of total RNA, treated with T4 DNA polymerase, and
                      purified by ethanol-precipitation. The cDNAs were ligated
                      to Lone-linker LL-Sal4, purified by phenol/chloroform, and
                      separated from free linkers by Centricon 100. Then, the
                      cDNAs were amplified by long-range high fidelity PCR using
                      Ex Taq polymerase (Takara) with a primer Sal4-S. The
                      products were purified by phenol/chloroform and Centricon
                      100. The cDNAs were digested with SalI and NotI enzymes
                      and cloned into SalI/NotI site of pCMV-SPORT6 plasmid
                      vector. The DH10B E. coli host was transformed with the
                      ligation mixture by the standard chemical method. The
                      average insert size is about 3.4Kb. The library was
                      constructed by Yulan Piao."
ORIGIN

Alignment Scores:
Pred. No.:                5.47           Length:          493
Score:                    10.00          Matches:         10
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              62.50%         Indels:          0
DB:                       7              Gaps:            0

US-10-726-967A-3 (1-16) x CN692524 (1-493)

Qy          4 GlyIleArgLeuProLeuArgSerGlyLeu 13
              |||||||||||||||||||||||||||||
Db        382 GGCATCCGGCTGCCCCTTCGCAGCGGCCTG 411

RESULT 8
CN697484
LOCUS       CN697484                 533 bp    mRNA    linear   EST 18-MAY-2004
DEFINITION  E0394H10-5 NIA Mouse E10.5 whole embryo cDNA library (Long) Mus
            musculus cDNA clone NIA:E0394H10 IMAGE:30868029 5', mRNA sequence.
ACCESSION   CN697484
VERSION     CN697484.1  GI:47466233
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 533)
  AUTHORS   Sharov,A.A., Piao,Y., Matoba,R., Dudekula,D.B., Qian,Y.,
            VanBuren,V., Falco,G., Martin,P.R., Stagg,C.A., Bassey,U.C.,
            Wang,Y., Carter,M.G., Hamatani,T., Aiba,K., Akutsu,H., Sharova,L.,
            Tanaka,T.S., Kimber,W.L., Yoshikawa,T., Jaradat,S.A., Pantano,S.,
            Nagaraja,R., Boheler,K.R., Taub,D., Hodes,R.J., Longo,D.L.,
            Schlessinger,D., Keller,J., Klotz,E., Kelsoe,G., Umezawa,A.,
            Vescovi,A.L., Rossant,J., Kunath,T., Hogan,B.L., Curci,A.,
            D'Urso,M., Kelso,J., Hide,W. and Ko,M.S.
  TITLE     Transcriptome analysis of mouse stem cells and early embryos
  JOURNAL   PLoS Biol. 1 (3), 410-419 (2003)
COMMENT     Contact: Dawood B. Dudekula
            Laboratory of Genetics
            National Institute on Aging/National Institutes of Health
            333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
            Email: cdna@lgsun.grc.nia.nih.gov
            Plate: E0394  row: H  column: 10
            Seq primer: M13 Reverse
            High quality sequence stop: 533
            POLYA=No.
```

```
FEATURES             Location/Qualifiers
     source          1. .533
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="niaEST:E0394H10-5"
                     /db_xref="taxon:10090"
                     /clone="NIA:E0394H10 IMAGE:30868029"
                     /tissue_type="whole embryo including extraembryonic
                     tissues at 10.5-days postcoitum"
                     /dev_stage="E10.5"
                     /lab_host="DH10B"
                     /clone_lib="NIA Mouse E10.5 whole embryo cDNA library
                     (Long)"
                     /note="Vector: pCMV-SPORT6 (Invitrogen); Site_1: SalI;
                     Site_2: NotI; Mouse cDNA project by the Laboratory of
                     Genetics, National Institute on Aging (NIA), Intramural
                     Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA).
                     This is a long-transcript enriched cDNA library (Ref.
                     Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total
                     RNAs were extracted from a pool of 8 embryos at 10.5-days
                     postcoitum. Double-stranded cDNAs were synthesized with an
                     Oligo(dT) primer [Invitrogen:
                     5'-pGACTAGTTCTAGATCGCGAGCGGCCGCCCTTTTTTTTTTTTTTT-3'] from
                     2ug of total RNA, treated with T4 DNA polymerase, and
                     purified by ethanol-precipitation. The cDNAs were ligated
                     to Lone-linker LL-Sal4, purified by phenol/chloroform, and
                     separated from free linkers by Centricon 100. Then, the
                     cDNAs were amplified by long-range high fidelity PCR using
                     Ex Taq polymerase (Takara) with a primer Sal4-S. The
                     products were purified by phenol/chloroform and Centricon
                     100. The cDNAs were digested with SalI and NotI enzymes
                     and cloned into SalI/NotI site of pCMV-SPORT6 plasmid
                     vector. The DH10B E. coli host was transformed with the
                     ligation mixture by the standard chemical method. The
                     average insert size is about 3.4Kb. The library was
                     constructed by Yulan Piao."
ORIGIN

Alignment Scores:
Pred. No.:                5.87          Length:          533
Score:                    10.00         Matches:         10
Percent Similarity:       100.00%       Conservative:    0
Best Local Similarity:    100.00%       Mismatches:      0
Query Match:              62.50%        Indels:          0
DB:                       7             Gaps:            0

US-10-726-967A-3 (1-16) x CN697484 (1-533)

Qy          4 GlyIleArgLeuProLeuArgSerGlyLeu 13
              ||||||||||||||||||||||||||||||||
Db        504 GGCATCCGGCTGCCCCTTCGCAGCGGCCTG 533

RESULT 9
CF903755
LOCUS       CF903755                 547 bp    mRNA    linear   EST 04-NOV-2003
DEFINITION  A0413D10-5 NIA Mouse Osteoblast cDNA Library (Long 1) Mus musculus
            cDNA clone NIA:A0413D10 IMAGE:30739245 5', mRNA sequence.
ACCESSION   CF903755
VERSION     CF903755.1  GI:38170804
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 547)
  AUTHORS   Piao,Y., Ko,N.T., Lim,M.K. and Ko,M.S.H.
  TITLE     Construction of long-transcript enriched cDNA libraries from
            submicrogram amounts of total RNAs by a universal PCR amplification
            method
  JOURNAL   Genome Res. 11 (9), 1553-1558 (2001)
  MEDLINE   21429098
   PUBMED   11544199
```

```
COMMENT     Contact: Dawood B. Dudekula
            Laboratory of Genetics
            National Institute on Aging/National Institutes of Health
            333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
            Email: cdna@lgsun.grc.nia.nih.gov
            Plate: A0413  row: D  column: 10
            Seq primer: M13 Reverse
            High quality sequence stop: 547
            POLYA=No.
FEATURES             Location/Qualifiers
     source          1. .547
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C3H/He mice"
                     /db_xref="niaEST:A0413D10-5"
                     /db_xref="taxon:10090"
                     /clone="NIA:A0413D10 IMAGE:30739245"
                     /dev_stage="KUSA/A1 cells"
                     /lab_host="DH10B"
                     /clone_lib="NIA Mouse Osteoblast cDNA Library (Long 1)"
                     /note="Vector: pCMV-SPORT6 (Invitrogen); Site_1: SalI;
                     Site_2: NotI; Mouse cDNA project by the Laboratory of
                     Genetics, National Institute on Aging (NIA), Intramural
                     Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA).
                     This is a long-transcript enriched cDNA library (Ref.
                     Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total
                     RNAs were obtained from Dr. Akihiro Umezawa (Keio
                     University School of Medicine, Japan). Double-stranded
                     cDNAs were synthesized with an Oligo(dT) primer
                     [Invitrogen:
                     5'-pGACTAGTTCTAGATCGCGAGCGGCCGCCCTTTTTTTTTTTTTTT-3'] from
                     2.1 ug of total RNA, treated with T4 DNA polymerase, and
                     purified by ethanol-precipitation. The cDNAs were ligated
                     to Lone-linker LL-Sal4, purified by phenol/chloroform, and
                     separated from free linkers by Centricon 100. Then, the
                     cDNAs were amplified by long-range high fidelity PCR using
                     Ex Taq polymerase (Takara) with a primer Sal4-S. The
                     products were purified by phenol/chloroform and Centricon
                     100. The cDNAs were digested with SalI and NotI enzymes
                     and cloned into SalI/NotI site of pCMV-SPORT6 plasmid
                     vector. The DH10B E. coli host was transformed with the
                     ligation mixture by the standard chemical method. The
                     average insert size is about 3.0 kb. The library was
                     constructed by Yulan Piao."
ORIGIN

Alignment Scores:
Pred. No.:                6             Length:          547
Score:                    10.00         Matches:         10
Percent Similarity:       100.00%       Conservative:    0
Best Local Similarity:    100.00%       Mismatches:      0
Query Match:              62.50%        Indels:          0
DB:                       7             Gaps:            0

US-10-726-967A-3 (1-16) x CF903755 (1-547)

Qy          4 GlyIleArgLeuProLeuArgSerGlyLeu 13
              ||||||||||||||||||||||||||||||||
Db        497 GGCATCCGGCTGCCCCTTCGCAGCGGCCTG 526

RESULT 10
CF906581
LOCUS       CF906581                 563 bp    mRNA    linear   EST 04-NOV-2003
DEFINITION  A0448H07-5 NIA Mouse Osteoblast cDNA Library (Long 1) Mus musculus
            cDNA clone NIA:A0448H07 IMAGE:30742650 5', mRNA sequence.
ACCESSION   CF906581
VERSION     CF906581.1  GI:38173630
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 563)
```

AUTHORS Piao,Y., Ko,N.T., Lim,M.K. and Ko,M.S.H.
TITLE Construction of long-transcript enriched cDNA libraries from submicrogram amounts of total RNAs by a universal PCR amplification method
JOURNAL Genome Res. 11 (9), 1553-1558 (2001)
MEDLINE 21429098
PUBMED 11544199
COMMENT Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov
Plate: A0448 row: H column: 07
Seq primer: M13 Reverse
High quality sequence stop: 563
POLYA=No.

FEATURES Location/Qualifiers
source 1. .563
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C3H/He mice"
/db_xref="niaEST:A0448H07-5"
/db_xref="taxon:10090"
/clone="NIA:A0448H07 IMAGE:30742650"
/dev_stage="KUSA/A1 cells"
/lab_host="DH10B"
/clone_lib="NIA Mouse Osteoblast cDNA Library (Long 1)"
/note="Vector: pCMV-SPORT6 (Invitrogen); Site_1: SalI; Site_2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were obtained from Dr. Akihiro Umezawa (Keio University School of Medicine, Japan). Double-stranded cDNAs were synthesized with an Oligo(dT) primer [Invitrogen: 5'-pGACTAGTTCTAGATCGCGAGCGGCCGCCCTTTTTTTTTTTTTTT-3'] from 2.1 ug of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to Lone-linker LL-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pCMV-SPORT6 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 3.0 kb. The library was constructed by Yulan Piao."

ORIGIN

Alignment Scores:

Pred. No.:	6.16	Length:	563
Score:	10.00	Matches:	10
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	62.50%	Indels:	0
DB:	7	Gaps:	0

US-10-726-967A-3 (1-16) x CF906581 (1-563)

```
Qy          4 GlyIleArgLeuProLeuArgSerGlyLeu 13
              ||||||||||||||||||||||||||||||
Db        497 GGCATCCGGCTGCCCCTTCGCAGCGGCCTG 526
```

RESULT 11
CF171218
LOCUS CF171218 576 bp mRNA linear EST 25-JUL-2003
DEFINITION B0839F04-5 NIA Mouse Newborn Kidney cDNA Library (Long 1) Mus musculus cDNA clone NIA:B0839F04 IMAGE:30471231 5', mRNA sequence.
ACCESSION CF171218
VERSION CF171218.1 GI:33280767
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 576)
AUTHORS Piao,Y., Ko,N.T., Lim,M.K. and Ko,M.S.H.
TITLE Construction of long-transcript enriched cDNA libraries from submicrogram amounts of total RNAs by a universal PCR amplification method
JOURNAL Genome Res. 11 (9), 1553-1558 (2001)
MEDLINE 21429098
PUBMED 11544199
COMMENT Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov
Plate: B0839 row: F column: 04
Seq primer: M13 Reverse
High quality sequence stop: 576
POLYA=No.

FEATURES Location/Qualifiers
source 1. .576
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="niaEST:B0839F04-5"
/db_xref="taxon:10090"
/clone="NIA:B0839F04 IMAGE:30471231"
/dev_stage="Newborn Kidney"
/lab_host="DH10B"
/clone_lib="NIA Mouse Newborn Kidney cDNA Library (Long 1)"
/note="Vector: pCMV-SPORT6 (Invitrogen); Site_1: SalI; Site_2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). In brief, double-stranded cDNAs were synthesized with an Oligo(dT) primer [Invitrogen: 5'-pGACTAGTTCTAGATCGCGAGCGGCCGCCCTTTTTTTTTTTTTTT-3'] from 26 ug of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to Lone-linker LL-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pCMV-SPORT6 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 3.0 kb. The library was constructed by Yulan Piao."

ORIGIN

Alignment Scores:

Pred. No.:	6.29	Length:	576
Score:	10.00	Matches:	10
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	62.50%	Indels:	0
DB:	7	Gaps:	0

US-10-726-967A-3 (1-16) x CF171218 (1-576)

```
Qy          4 GlyIleArgLeuProLeuArgSerGlyLeu 13
              ||||||||||||||||||||||||||||||
Db        497 GGCATCCGGCTGCCCCTTCGCAGCGGCCTG 526
```

RESULT 12
BY713879

```
LOCUS       BY713879                600 bp    mRNA    linear   EST 17-DEC-2002
DEFINITION  BY713879 RIKEN full-length enriched, 16 days embryo head Mus
            musculus cDNA clone 4122401C04 5', mRNA sequence.
ACCESSION   BY713879
VERSION     BY713879.1  GI:27126044
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 600)
  AUTHORS   Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
            Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
            Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
            Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,
            Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,
            Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,
            Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,
            Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,
            Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,
            Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,
            Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A.,
            Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,
            Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,
            Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G.,
            Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S.,
            Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,
            Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K.,
            Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,
            Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y.,
            Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I.,
            Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,
            Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M.,
            Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,
            Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y.,
            Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.,
            Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,
            Rogers,J., Birney,E. and Hayashizaki,Y.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
  MEDLINE   22354683
   PUBMED   12466851
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
            Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P.,
            Fukuda,S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F.,
            Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y.,
            Kondo,S., Konno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M.,
            Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Saito,R., Sakazume,N.,
            Sano,H., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M.,
            Takeda,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.
            Direct Submission
             Computational Analysis of Full-Length Mouse cDNAs Compared with
            Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
             Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new
            genes. Genome Res. 10 (10), 1617-1630 (2000)
             RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer. Genome Res.
            10 (11), 1757-1771 (2000)
             Computer-based methods for the mouse full-length cDNA
            encyclopedia: real-time sequence clustering for construction of a
            nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
             cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
             Please visit our web site (http://genome.gsc.riken.go.jp) for
            further details.
FEATURES             Location/Qualifiers
     source          1. .600
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="4122401C04"
                     /sex="mixed"
                     /tissue_type="head"
                     /dev_stage="16 days embryo"
                     /lab_host="DH10B"
                     /clone_lib="RIKEN full-length enriched, 16 days embryo
                     head"
                     /note="Site_1: SalI; Site_2: BamHI; cDNA library was
                     prepared and sequenced in Mouse Genome Encyclopedia
                     Project of Genome Exploration Research Group in Riken
                     Genomic Sciences Center and Genome Science Laboratory in
                     RIKEN. Division of Experimental Animal Research in Riken
                     contributed to prepare mouse tissues. 1st strand cDNA was
                     primed with a primer [5'
                     GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was
                     prepared by using trehalose thermo-activated reverse
                     transcriptase and subsequently enriched for full-length by
                     cap-trapper. Second strand cDNA was prepared with the
                     primer adapter of sequence [5'
                     GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCCC 3']. cDNA
                     was cloned into the XhoI and BamHI sites. Vector: a
                     modified pBluescript KS(+) after bulk excision from Lambda
                     FLC I"
ORIGIN

Alignment Scores:
Pred. No.:                  6.52          Length:          600
Score:                      10.00         Matches:         10
Percent Similarity:         100.00%       Conservative:    0
Best Local Similarity:      100.00%       Mismatches:      0
Query Match:                62.50%        Indels:          0
DB:                         6             Gaps:            0

US-10-726-967A-3 (1-16) x BY713879 (1-600)

Qy          4 GlyIleArgLeuProLeuArgSerGlyLeu 13
              |||||||||||||||||||||||||||||||
Db        498 GGCATCCGGCTGCCCCTTCGCAGCGGCCTG 527

RESULT 13
BB644736
LOCUS       BB644736                619 bp    mRNA    linear   EST 26-OCT-2001
DEFINITION  BB644736 RIKEN full-length enriched, adult male corpora
            quadrigemina Mus musculus cDNA clone B230346M13 5', mRNA sequence.
ACCESSION   BB644736
VERSION     BB644736.1  GI:16479273
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 619)
  AUTHORS   Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T.,
            Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J.,
            Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K.,
            Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K.,
            Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,
            Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.
  TITLE     RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
```

Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. . 10 (11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001)
Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and Hayashizaki,Y.
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
e mouse tissues.

FEATURES Location/Qualifiers
source 1. .619
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="B230346M13"
/sex="male"
/tissue_type="corpora quadrigemina"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="RIKEN full-length enriched, adult male corpora quadrigemina"
/note="Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 20.0 and subtraction to Rot = 459.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."

ORIGIN

Alignment Scores:

Pred. No.:	6.7	Length:	619
Score:	10.00	Matches:	10
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	62.50%	Indels:	0
DB:	2	Gaps:	0

US-10-726-967A-3 (1-16) x BB644736 (1-619)

Qy 4 GlyIleArgLeuProLeuArgSerGlyLeu 13
||||||||||||||||||||||||||||
Db 516 GGCATCCGGCTGCCCCTTCGCAGCGGCCTG 545

RESULT 14
CD348605
LOCUS CD348605 637 bp mRNA linear EST 09-JUL-2003
DEFINITION UI-M-FY0-cfo-g-02-0-UI.r1 NIH_BMAP_FY0 Mus musculus cDNA clone IMAGE:6853755 5', mRNA sequence.
ACCESSION CD348605
VERSION CD348605.1 GI:31140120
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 637)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at http://genome.uiowa.edu/distribution/mousefl.html
This clone was contributed by the Brain Molecular Anatomy Project (BMAP)
Seq primer: pYX-5.

FEATURES Location/Qualifiers
source 1. .637
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:6853755"
/tissue_type="whole brain"
/dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH_BMAP_FY0"
/note="Organ: Brain; Vector: pYX- Asc; Site_1: EcoR I; Site_2: Not I; The library was constructed according Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is AGCGAGACAG. This library was created for the University Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

ORIGIN

Alignment Scores:

Pred. No.:	6.87	Length:	637
Score:	10.00	Matches:	10
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	62.50%	Indels:	0
DB:	6	Gaps:	0

US-10-726-967A-3 (1-16) x CD348605 (1-637)

Qy 4 GlyIleArgLeuProLeuArgSerGlyLeu 13
||||||||||||||||||||||||||||
Db 498 GGCATCCGGCTGCCCCTTCGCAGCGGCCTG 527

RESULT 15

```
BB632244
LOCUS       BB632244                639 bp    mRNA    linear   EST 26-OCT-2001
DEFINITION  BB632244 RIKEN full-length enriched, adult male hypothalamus Mus
            musculus cDNA clone A230019C07 5', mRNA sequence.
ACCESSION   BB632244
VERSION     BB632244.1  GI:16468863
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 639)
  AUTHORS   Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T.,
            Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J.,
            Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K.,
            Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K.,
            Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,
            Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.
  TITLE     RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
            Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
             Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new
            genes. Genome Res. . 10 (10), 1617-1630 (2000)
             wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
            Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,
            Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A.
            and Hayashizaki,Y.
             RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer. Genome Res.
            10 (11), 1757-1771 (2000)
             Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P.,
            Sugahara,Y. and Hayashizaki,Y.
             Computer-based methods for the mouse full-length cDNA
            encyclopedia: real-time sequence clustering for construction of a
            nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001)
             Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I.,
            Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
            Hayashizaki,Y.
             Computational Analysis of Full-Length Mouse cDNAs Compared with
            Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
             Please visit our web site (http://genome.gsc.riken.go.jp) for
            further details.
             e mouse tissues.
FEATURES             Location/Qualifiers
     source          1. .639
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10090"
                     /clone="A230019C07"
                     /sex="male"
                     /tissue_type="hypothalamus"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /clone_lib="RIKEN full-length enriched, adult male
                     hypothalamus"
                     /note="Site_1: SalI; Site_2: BamHI; cDNA library was
                     prepared and sequenced in Mouse Genome Encyclopedia
                     Project of Genome Exploration Research Group in Riken
                     Genomic Sciences Center and Genome Science Laboratory in
                     RIKEN. Division of Experimental Animal Research in Riken
                     contributed to prepare mouse tissues. 1st strand cDNA was
                     primed with a primer [5'
                     GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was
                     prepared by using trehalose thermo-activated reverse
                     transcriptase and subsequently enriched for full-length by
                     cap-trapper. cDNA went through one round of normalization
                     to Rot = 20.0 and subtraction to Rot = 459.0. Second
                     strand cDNA was prepared with the primer adapter of
                     sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCC
                     3']. cDNA was cleaved with XhoI and BamHI. Vector: a
                     modified pBluescript KS(+) after bulk excision from Lambda
                     FLC I. "
ORIGIN

Alignment Scores:
Pred. No.:                6.89          Length:          639
Score:                    10.00         Matches:         10
Percent Similarity:       100.00%       Conservative:    0
Best Local Similarity:    100.00%       Mismatches:      0
Query Match:              62.50%        Indels:          0
DB:                       2             Gaps:            0

US-10-726-967A-3 (1-16) x BB632244 (1-639)

Qy          4 GlyIleArgLeuProLeuArgSerGlyLeu 13
              ||||||||||||||||||||||||||||
Db        518 GGCATCCGGCTGCCCCTTCGCAGCGGCCTG 547


Search completed: July 27, 2005, 20:35:53
Job time : 3150 secs
```

GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: July 27, 2005, 16:41:37 ; Search time 1935 Seconds
(without alignments)
701.161 Million cell updates/sec

Title: US-10-726-967A-52
Perfect score: 144
Sequence: 1 GYYVEMTVGSPPQTLNILVDTGSSNFAV 28

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US10726967/runat_26072005_130734_6141/app_query.fasta_1.199
-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10726967_@CGN_1_1_5600_@runat_26072005_130734_6141 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	144	100.0	517	9	AB089958	AB089958 Homo sapi
2	144	100.0	1278	6	BD235898	BD235898 Alzheimer
3	144	100.0	1278	6	AR224104	AR224104 Sequence
4	144	100.0	1278	6	AR269235	AR269235 Sequence
5	144	100.0	1278	6	AR478790	AR478790 Sequence
6	144	100.0	1278	6	AR487356	AR487356 Sequence
7	144	100.0	1278	6	AR531996	AR531996 Sequence
8	144	100.0	1278	6	AR540897	AR540897 Sequence
9	144	100.0	1278	6	AR560107	AR560107 Sequence
10	144	100.0	1278	6	AX105409	AX105409 Sequence
11	144	100.0	1278	6	AX573847	AX573847 Sequence
12	144	100.0	1287	6	AR224122	AR224122 Sequence
13	144	100.0	1287	6	AR269253	AR269253 Sequence
14	144	100.0	1287	6	AR478808	AR478808 Sequence
15	144	100.0	1287	6	AR487374	AR487374 Sequence
16	144	100.0	1287	6	AR532014	AR532014 Sequence
17	144	100.0	1287	6	AR540915	AR540915 Sequence
18	144	100.0	1287	6	AR560125	AR560125 Sequence
19	144	100.0	1287	6	AX105432	AX105432 Sequence
20	144	100.0	1287	6	AX573870	AX573870 Sequence
21	144	100.0	1302	6	BD235897	BD235897 Alzheimer
22	144	100.0	1302	6	AR224103	AR224103 Sequence
23	144	100.0	1302	6	AR269234	AR269234 Sequence
24	144	100.0	1302	6	AR478789	AR478789 Sequence
25	144	100.0	1302	6	AR487355	AR487355 Sequence
26	144	100.0	1302	6	AR531995	AR531995 Sequence
27	144	100.0	1302	6	AR540896	AR540896 Sequence
28	144	100.0	1302	6	AR560106	AR560106 Sequence
29	144	100.0	1302	6	AX105407	AX105407 Sequence
30	144	100.0	1302	6	AX573845	AX573845 Sequence
31	144	100.0	1302	6	AX700454	AX700454 Sequence
32	144	100.0	1305	6	AR224123	AR224123 Sequence
33	144	100.0	1305	6	AR269254	AR269254 Sequence
34	144	100.0	1305	6	AR478809	AR478809 Sequence
35	144	100.0	1305	6	AR487375	AR487375 Sequence
36	144	100.0	1305	6	AR532015	AR532015 Sequence
37	144	100.0	1305	6	AR540916	AR540916 Sequence
38	144	100.0	1305	6	AR560126	AR560126 Sequence
39	144	100.0	1305	6	AX105434	AX105434 Sequence
40	144	100.0	1305	6	AX573872	AX573872 Sequence
41	144	100.0	1333	9	AB050438	AB050438 Homo sapi
42	144	100.0	1341	6	BD235895	BD235895 Alzheimer
43	144	100.0	1341	6	AR224101	AR224101 Sequence
44	144	100.0	1341	6	AR269232	AR269232 Sequence
45	144	100.0	1341	6	AR478787	AR478787 Sequence

ALIGNMENTS

RESULT 1
AB089958
LOCUS AB089958 517 bp mRNA linear PRI 19-AUG-2003
DEFINITION Homo sapiens BACE mRNA for beta-site APP cleaving enzyme isoform I-127, complete cds.
ACCESSION AB089958
VERSION AB089958.1 GI:34014375
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Tanahashi,H.
TITLE A novel alternatively spliced isoform of BACE, I-127 induced by cycloheximide treatment
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 517)
AUTHORS Tanahashi,H.
TITLE Direct Submission
JOURNAL Submitted (17-AUG-2002) Hiroshi Tanahashi, National Institute of Neuroscience, Division of Demyelinating Disease and Aging; 4-1-1 Ogawahigashi, Kodaira, Tokyo 187-8502, Japan
(E-mail:tanahash@ncnp.go.jp, Tel:81-042-341-2711(ex.5163), Fax:81-042-346-1747)
FEATURES Location/Qualifiers
source 1. .517
/organism="Homo sapiens"

```
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /chromosome="11"
                     /map="11q23.2-23.3"
                     /cell_line="human neuroblastoma SH-SY5Y"
                     /note="I-127 is induced by cycloheximide treatment.
                     Alternative splicing of the RNA occurs at an internal
                     donor in exon 3."
     gene            1. .517
                     /gene="BACE"
     CDS             1. .384
                     /gene="BACE"
                     /codon_start=1
                     /product="beta-site APP cleaving enzyme isoform I-127"
                     /protein_id="BAC81826.1"
                     /db_xref="GI:34014376"
                     /translation="MAQALPWLLLWMGAGVLPAHGTQHGIRLPLRSGLGGAPLGLRLP
                     RETDEEPEEPGRRGSFVEMVDNLRGKSGQGYYVEMTVGSPPQTLNILVDTGSSNFAVG
                     AAPHPFLHRYYQRQLSSTYRDLRKA"
ORIGIN

Alignment Scores:
Pred. No.:                1.13e-14        Length:         517
Score:                    144.00          Matches:        28
Percent Similarity:       100.00%         Conservative:   0
Best Local Similarity:    100.00%         Mismatches:     0
Query Match:              100.00%         Indels:         0
DB:                       9               Gaps:           0

US-10-726-967A-52 (1-28) x AB089958 (1-517)

Qy          1 GlyTyrTyrValGluMetThrValGlySerProProGlnThrLeuAsnIleLeuValAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        220 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGAT 279

Qy         21 ThrGlySerSerAsnPheAlaVal 28
              ||||||||||||||||||||||||||
Db        280 ACAGGCAGCAGTAACTTTGCAGTG 303

RESULT 2
BD235898
LOCUS       BD235898                1278 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Alzheimer's disease secretase.
ACCESSION   BD235898
VERSION     BD235898.1  GI:33045668
KEYWORDS    JP 2002526081-A/14.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1278)
  AUTHORS   Gurney,M.E., Bienkowski,M.J., Heinrikson,R.L., Parodi,L.A. and
            Yan,R.
  TITLE     Alzheimer's disease secretase
  JOURNAL   Patent: JP 2002526081-A 14 20-AUG-2002;
            PHARMACIA AND UPJOHN CO
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002526081-A/14
            PD   20-AUG-2002
            PF   23-SEP-1999 JP 2000574268
            PR   24-SEP-1998 US    60/101594
            PI   MARK E GURNEY,MICHAEL JEROME BIENKOWSKI,ROBERT LEROY  PI
            HEINRIKSON,
            PI   LUIS A PARODI,RIQIANG YAN
            PC   C12N15/09,A61K45/00,A61P25/28,C07K14/47,C07K16/18,C12N1/15, PC
              C12N1/19,
            PC
            C12N1/21,C12N5/10,C12N9/64,C12P21/02,C12P21/08,C12Q1/37,G01N33/ PC
             15,
            PC   G01N33/50//(C12N1/21,C12R1:19),C12N15/00,C12N5/00 CC
            Alzheimer's disease secretase
            FH   Key             Location/Qualifiers
            FT   source          1. .1278
            FT                   /organism='Homo sapiens (human)'.
FEATURES                Location/Qualifiers
     source             1. .1278
                        /organism="Homo sapiens"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:9606"
ORIGIN

Alignment Scores:
Pred. No.:                3.18e-14        Length:         1278
Score:                    144.00          Matches:        28
Percent Similarity:       100.00%         Conservative:   0
Best Local Similarity:    100.00%         Mismatches:     0
Query Match:              100.00%         Indels:         0
DB:                       6               Gaps:           0

US-10-726-967A-52 (1-28) x BD235898 (1-1278)

Qy          1 GlyTyrTyrValGluMetThrValGlySerProProGlnThrLeuAsnIleLeuValAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGAT 195

Qy         21 ThrGlySerSerAsnPheAlaVal 28
              ||||||||||||||||||||||||||
Db        196 ACAGGCAGCAGTAACTTTGCAGTG 219

RESULT 3
AR224104
LOCUS       AR224104                1278 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 27 from patent US 6440698.
ACCESSION   AR224104
VERSION     AR224104.1  GI:23332764
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1278)
  AUTHORS   Gurney,M.E., Bienkowski,M.J., Heinrikson,R.L., Parodi,L.A. and
            Yan,R.
  TITLE     Alzheimer's disease secretase, APP substrates therefor, and uses
            therefor
  JOURNAL   Patent: US 6440698-A 27 27-AUG-2002;
FEATURES                Location/Qualifiers
     source             1. .1278
                        /organism="unknown"
                        /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:                3.18e-14        Length:         1278
Score:                    144.00          Matches:        28
Percent Similarity:       100.00%         Conservative:   0
Best Local Similarity:    100.00%         Mismatches:     0
Query Match:              100.00%         Indels:         0
DB:                       6               Gaps:           0

US-10-726-967A-52 (1-28) x AR224104 (1-1278)

Qy          1 GlyTyrTyrValGluMetThrValGlySerProProGlnThrLeuAsnIleLeuValAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGAT 195

Qy         21 ThrGlySerSerAsnPheAlaVal 28
              ||||||||||||||||||||||||||
Db        196 ACAGGCAGCAGTAACTTTGCAGTG 219

RESULT 4
AR269235
LOCUS       AR269235                1278 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 27 from patent US 6500667.
ACCESSION   AR269235
VERSION     AR269235.1  GI:29700203
KEYWORDS    .
```

```
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1278)
  AUTHORS   Gurney,M.E., Bienkowski,M.J., Heinrikson,R.L., Parodi,L.A. and
            Yan,R.
  TITLE     Aspartyl protease 2 (Asp2) antisense oligonucleotides
  JOURNAL   Patent: US 6500667-A 27 31-DEC-2002;
FEATURES             Location/Qualifiers
     source          1. .1278
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              3.18e-14        Length:         1278
Score:                  144.00          Matches:        28
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     6               Gaps:           0

US-10-726-967A-52 (1-28) x AR269235 (1-1278)

Qy          1 GlyTyrTyrValGluMetThrValGlySerProProGlnThrLeuAsnIleLeuValAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGAT 195

Qy         21 ThrGlySerSerAsnPheAlaVal 28
              |||||||||||||||||||||||||
Db        196 ACAGGCAGCAGTAACTTTGCAGTG 219

RESULT 5
AR478790
LOCUS       AR478790                1278 bp    DNA     linear   PAT 14-MAY-2004
DEFINITION  Sequence 27 from patent US 6699671.
ACCESSION   AR478790
VERSION     AR478790.1  GI:47237510
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1278)
  AUTHORS   Gurney,M.E., Bienkowski,M.J., Heinrikson,R.L., Parodi,L.A. and
            Yan,R.
  TITLE     Alzheimer's disease secretase, APP substrates therefor, and uses
            therefor
  JOURNAL   Patent: US 6699671-A 27 02-MAR-2004;
FEATURES             Location/Qualifiers
     source          1. .1278
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              3.18e-14        Length:         1278
Score:                  144.00          Matches:        28
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     6               Gaps:           0

US-10-726-967A-52 (1-28) x AR478790 (1-1278)

Qy          1 GlyTyrTyrValGluMetThrValGlySerProProGlnThrLeuAsnIleLeuValAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGAT 195

Qy         21 ThrGlySerSerAsnPheAlaVal 28
              |||||||||||||||||||||||||
Db        196 ACAGGCAGCAGTAACTTTGCAGTG 219

RESULT 6
AR487356
LOCUS       AR487356                1278 bp    DNA     linear   PAT 14-MAY-2004
DEFINITION  Sequence 27 from patent US 6706485.
ACCESSION   AR487356
VERSION     AR487356.1  GI:47252454
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1278)
  AUTHORS   Gurney,M.E., Bienkowski,M.J., Heinrikson,R.L., Parodi,L.A. and
            Yan,R.
  TITLE     Method of identifying agents that inhibit APP processing activity
  JOURNAL   Patent: US 6706485-A 27 16-MAR-2004;
FEATURES             Location/Qualifiers
     source          1. .1278
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              3.18e-14        Length:         1278
Score:                  144.00          Matches:        28
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     6               Gaps:           0

US-10-726-967A-52 (1-28) x AR487356 (1-1278)

Qy          1 GlyTyrTyrValGluMetThrValGlySerProProGlnThrLeuAsnIleLeuValAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGAT 195

Qy         21 ThrGlySerSerAsnPheAlaVal 28
              |||||||||||||||||||||||||
Db        196 ACAGGCAGCAGTAACTTTGCAGTG 219

RESULT 7
AR531996
LOCUS       AR531996                1278 bp    DNA     linear   PAT 08-OCT-2004
DEFINITION  Sequence 27 from patent US 6727074.
ACCESSION   AR531996
VERSION     AR531996.1  GI:53920530
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1278)
  AUTHORS   Gurney,M.E., Bienkowski,M.J., Heinrikson,R.L., Parodi,L.A. and
            Yan,R.
  TITLE     Alzheimer's disease secretase, APP substrates therefor, and uses
            therefor
  JOURNAL   Patent: US 6727074-A 27 27-APR-2004;
FEATURES             Location/Qualifiers
     source          1. .1278
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              3.18e-14        Length:         1278
Score:                  144.00          Matches:        28
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     6               Gaps:           0

US-10-726-967A-52 (1-28) x AR531996 (1-1278)

Qy          1 GlyTyrTyrValGluMetThrValGlySerProProGlnThrLeuAsnIleLeuValAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGAT 195
```

```
Qy         21 ThrGlySerSerAsnPheAlaVal 28
              ||||||||||||||||||||||||
Db        196 ACAGGCAGCAGTAACTTTGCAGTG 219

RESULT 8
AR540897
LOCUS       AR540897                1278 bp    DNA     linear   PAT 08-OCT-2004
DEFINITION  Sequence 27 from patent US 6737510.
ACCESSION   AR540897
VERSION     AR540897.1  GI:53932410
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1278)
  AUTHORS   Gurney,M.E., Bienkowski,M.J., Heinrikson,R.L., Parodi,L.A. and
            Yan,R.
  TITLE     Alzheimer's disease secretase, APP substrates therefor, and uses
            thereof
  JOURNAL   Patent: US 6737510-A 27 18-MAY-2004;
FEATURES             Location/Qualifiers
     source          1. .1278
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              3.18e-14        Length:         1278
Score:                  144.00          Matches:        28
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     6               Gaps:           0

US-10-726-967A-52 (1-28) x AR540897 (1-1278)

Qy          1 GlyTyrTyrValGluMetThrValGlySerProProGlnThrLeuAsnIleLeuValAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGAT 195

Qy         21 ThrGlySerSerAsnPheAlaVal 28
              ||||||||||||||||||||||||
Db        196 ACAGGCAGCAGTAACTTTGCAGTG 219

RESULT 9
AR560107
LOCUS       AR560107                1278 bp    DNA     linear   PAT 08-OCT-2004
DEFINITION  Sequence 27 from patent US 6753163.
ACCESSION   AR560107
VERSION     AR560107.1  GI:53970474
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1278)
  AUTHORS   Gurney,M.E., Bienkowski,M.J., Heinrikson,R.L., Parodi,L.A. and
            Yan,R.
  TITLE     Alzheimer's disease secretase, APP substrates therefor, and uses
            therefor
  JOURNAL   Patent: US 6753163-A 27 22-JUN-2004;
FEATURES             Location/Qualifiers
     source          1. .1278
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              3.18e-14        Length:         1278
Score:                  144.00          Matches:        28
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     6               Gaps:           0

US-10-726-967A-52 (1-28) x AR560107 (1-1278)

Qy          1 GlyTyrTyrValGluMetThrValGlySerProProGlnThrLeuAsnIleLeuValAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGAT 195

Qy         21 ThrGlySerSerAsnPheAlaVal 28
              ||||||||||||||||||||||||
Db        196 ACAGGCAGCAGTAACTTTGCAGTG 219

RESULT 10
AX105409
LOCUS       AX105409                1278 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 27 from Patent WO0123533.
ACCESSION   AX105409
VERSION     AX105409.1  GI:13921523
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Gurney,M. and Bienkowski,M.J.
  TITLE     Alzheimer's disease secretase, app substrates therefor, and uses
            therefor
  JOURNAL   Patent: WO 0123533-A 27 05-APR-2001;
            Pharmacia & Upjohn Company (US)
FEATURES             Location/Qualifiers
     source          1. .1278
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Alignment Scores:
Pred. No.:              3.18e-14        Length:         1278
Score:                  144.00          Matches:        28
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     6               Gaps:           0

US-10-726-967A-52 (1-28) x AX105409 (1-1278)

Qy          1 GlyTyrTyrValGluMetThrValGlySerProProGlnThrLeuAsnIleLeuValAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGAT 195

Qy         21 ThrGlySerSerAsnPheAlaVal 28
              ||||||||||||||||||||||||
Db        196 ACAGGCAGCAGTAACTTTGCAGTG 219

RESULT 11
AX573847
LOCUS       AX573847                1278 bp    DNA     linear   PAT 07-JAN-2003
DEFINITION  Sequence 27 from Patent EP1249498.
ACCESSION   AX573847
VERSION     AX573847.1  GI:27551489
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Gurney,M. and Bienkowski,M.J.
  TITLE     Alzheimer's disease secretase, app substrates therefor, and uses
            therefor
  JOURNAL   Patent: EP 1249498-A 27 16-OCT-2002;
            PHARMACIA & UPJOHN COMPANY (US)
FEATURES             Location/Qualifiers
     source          1. .1278
```

```
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Alignment Scores:
Pred. No.:              3.18e-14        Length:         1278
Score:                  144.00          Matches:        28
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     6               Gaps:           0

US-10-726-967A-52 (1-28) x AX573847 (1-1278)

Qy          1 GlyTyrTyrValGluMetThrValGlySerProProGlnThrLeuAsnIleLeuValAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGAT 195

Qy         21 ThrGlySerSerAsnPheAlaVal 28
              |||||||||||||||||||||||||
Db        196 ACAGGCAGCAGTAACTTTGCAGTG 219

RESULT 12
AR224122
LOCUS       AR224122                1287 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 50 from patent US 6440698.
ACCESSION   AR224122
VERSION     AR224122.1  GI:23332782
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1287)
  AUTHORS   Gurney,M.E., Bienkowski,M.J., Heinrikson,R.L., Parodi,L.A. and
            Yan,R.
  TITLE     Alzheimer's disease secretase, APP substrates therefor, and uses
            therefor
  JOURNAL   Patent: US 6440698-A 50 27-AUG-2002;
FEATURES             Location/Qualifiers
     source          1. .1287
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              3.2e-14         Length:         1287
Score:                  144.00          Matches:        28
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     6               Gaps:           0

US-10-726-967A-52 (1-28) x AR224122 (1-1287)

Qy          1 GlyTyrTyrValGluMetThrValGlySerProProGlnThrLeuAsnIleLeuValAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        220 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGAT 279

Qy         21 ThrGlySerSerAsnPheAlaVal 28
              |||||||||||||||||||||||||
Db        280 ACAGGCAGCAGTAACTTTGCAGTG 303

RESULT 13
AR269253
LOCUS       AR269253                1287 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 50 from patent US 6500667.
ACCESSION   AR269253
VERSION     AR269253.1  GI:29700221
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1287)
  AUTHORS   Gurney,M.E., Bienkowski,M.J., Heinrikson,R.L., Parodi,L.A. and
            Yan,R.
  TITLE     Aspartyl protease 2 (Asp2) antisense oligonucleotides
  JOURNAL   Patent: US 6500667-A 50 31-DEC-2002;
FEATURES             Location/Qualifiers
     source          1. .1287
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              3.2e-14         Length:         1287
Score:                  144.00          Matches:        28
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     6               Gaps:           0

US-10-726-967A-52 (1-28) x AR269253 (1-1287)

Qy          1 GlyTyrTyrValGluMetThrValGlySerProProGlnThrLeuAsnIleLeuValAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        220 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGAT 279

Qy         21 ThrGlySerSerAsnPheAlaVal 28
              |||||||||||||||||||||||||
Db        280 ACAGGCAGCAGTAACTTTGCAGTG 303

RESULT 14
AR478808
LOCUS       AR478808                1287 bp    DNA     linear   PAT 14-MAY-2004
DEFINITION  Sequence 50 from patent US 6699671.
ACCESSION   AR478808
VERSION     AR478808.1  GI:47237528
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1287)
  AUTHORS   Gurney,M.E., Bienkowski,M.J., Heinrikson,R.L., Parodi,L.A. and
            Yan,R.
  TITLE     Alzheimer's disease secretase, APP substrates therefor, and uses
            therefor
  JOURNAL   Patent: US 6699671-A 50 02-MAR-2004;
FEATURES             Location/Qualifiers
     source          1. .1287
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              3.2e-14         Length:         1287
Score:                  144.00          Matches:        28
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     6               Gaps:           0

US-10-726-967A-52 (1-28) x AR478808 (1-1287)

Qy          1 GlyTyrTyrValGluMetThrValGlySerProProGlnThrLeuAsnIleLeuValAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        220 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGAT 279

Qy         21 ThrGlySerSerAsnPheAlaVal 28
              |||||||||||||||||||||||||
Db        280 ACAGGCAGCAGTAACTTTGCAGTG 303

RESULT 15
AR487374
LOCUS       AR487374                1287 bp    DNA     linear   PAT 14-MAY-2004
DEFINITION  Sequence 50 from patent US 6706485.
```

```
ACCESSION   AR487374
VERSION     AR487374.1  GI:47252472
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1287)
  AUTHORS   Gurney,M.E., Bienkowski,M.J., Heinrikson,R.L., Parodi,L.A. and
            Yan,R.
  TITLE     Method of identifying agents that inhibit APP processing activity
  JOURNAL   Patent: US 6706485-A 50 16-MAR-2004;
FEATURES             Location/Qualifiers
     source          1. .1287
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              3.2e-14        Length:          1287
Score:                  144.00         Matches:         28
Percent Similarity:     100.00%        Conservative:    0
Best Local Similarity:  100.00%        Mismatches:      0
Query Match:            100.00%        Indels:          0
DB:                     6              Gaps:            0

US-10-726-967A-52 (1-28) x AR487374 (1-1287)

Qy          1 GlyTyrTyrValGluMetThrValGlySerProProGlnThrLeuAsnIleLeuValAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        220 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGAT 279

Qy         21 ThrGlySerSerAsnPheAlaVal 28
              |||||||||||||||||||||||||
Db        280 ACAGGCAGCAGTAACTTTGCAGTG 303


Search completed: July 27, 2005, 18:50:18
Job time : 1939 secs
```

GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: July 27, 2005, 12:14:54 ; Search time 437 Seconds
(without alignments)
379.297 Million cell updates/sec

Title: US-10-726-967A-52
Perfect score: 144
Sequence: 1 GYYVEMTVGSPPQTLNILVDTGSSNFAV 28

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US10726967/runat_26072005_130733_6129/app_query.fasta_1.199
-DB=N_Geneseq_16Dec04 -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10726967_@CGN_1_1_708_@runat_26072005_130733_6129 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	144	100.0	1278	3	AAA15677	Aaa15677 Human Asp
2	144	100.0	1278	4	AAS11714	Aas11714 DNA encod
3	144	100.0	1278	4	AAD17877	Aad17877 T7-Caspas
4	144	100.0	1278	4	AAD13033	Aad13033 T7-Caspas
5	144	100.0	1278	4	AAD06751	Aad06751 T7-Caspas
6	144	100.0	1278	4	AAS11529	Aas11529 T7-Caspas
7	144	100.0	1278	6	ABL52469	Abl52469 T7-caspas
8	144	100.0	1278	12	ADJ94339	Adj94339 Human T7-
9	144	100.0	1278	12	ADO50435	Ado50435 T7-Caspas
10	144	100.0	1278	13	ADR75348	Adr75348 T7-Caspas
11	144	100.0	1287	4	AAD17895	Aad17895 Human-Asp
12	144	100.0	1287	4	AAD13276	Aad13276 Human-Asp
13	144	100.0	1287	4	AAD06768	Aad06768 Human asp
14	144	100.0	1287	4	AAS11547	Aas11547 Human cDN
15	144	100.0	1287	6	ABL52487	Abl52487 Human Asp
16	144	100.0	1287	12	ADJ94362	Adj94362 Human-pro
17	144	100.0	1287	12	ADO50458	Ado50458 Human Asp
18	144	100.0	1287	13	ADR75371	Adr75371 Human Asp
19	144	100.0	1302	3	AAA15670	Aaa15670 Human-pro
20	144	100.0	1302	4	AAS11713	Aas11713 DNA encod
21	144	100.0	1302	4	AAD17876	Aad17876 Human-pro
22	144	100.0	1302	4	AAD13032	Aad13032 Human-pro
23	144	100.0	1302	4	AAD06750	Aad06750 Human-pro
24	144	100.0	1302	4	AAS11528	Aas11528 Human cDN
25	144	100.0	1302	6	ABL52468	Abl52468 Human-pro
26	144	100.0	1302	12	ADJ94337	Adj94337 Human-pro
27	144	100.0	1302	12	ADO50433	Ado50433 Human-pro
28	144	100.0	1302	13	ADR75346	Adr75346 Human-pro
29	144	100.0	1305	4	AAS11733	Aas11733 DNA encod
30	144	100.0	1305	4	AAD17896	Aad17896 Human-Asp
31	144	100.0	1305	4	AAD13277	Aad13277 Human-Asp
32	144	100.0	1305	4	AAD06769	Aad06769 Human asp
33	144	100.0	1305	4	AAS11548	Aas11548 Human cDN
34	144	100.0	1305	6	ABL52488	Abl52488 Human Asp
35	144	100.0	1305	12	ADJ94364	Adj94364 Human-pro
36	144	100.0	1305	12	ADO50460	Ado50460 Human Asp
37	144	100.0	1305	13	ADR75373	Adr75373 Human Asp
38	144	100.0	1341	3	AAA15668	Aaa15668 T7-caspas
39	144	100.0	1341	4	AAS11711	Aas11711 DNA encod
40	144	100.0	1341	4	AAD17874	Aad17874 T7-Human-
41	144	100.0	1341	4	AAD13030	Aad13030 T7-Human-
42	144	100.0	1341	4	AAD06748	Aad06748 T7-Human-
43	144	100.0	1341	4	AAS11526	Aas11526 Human cDN
44	144	100.0	1341	6	ABL52466	Abl52466 T7-human-
45	144	100.0	1341	12	ADJ94333	Adj94333 Human cDN

ALIGNMENTS

RESULT 1
AAA15677
ID AAA15677 standard; DNA; 1278 BP.
XX
AC AAA15677;
XX
DT 03-AUG-2000 (first entry)
XX
DE Human Asp2 nucleotide sequence containing proteolytic cleavage site.
XX
KW Aspartyl protease; aspartase; amyloid precursor protein; APP; Asp 2;
KW Alzheimer's disease; beta secretase site; ss.
XX
OS Homo sapiens.
XX
PN WO200017369-A2.
XX
PD 30-MAR-2000.
XX
PF 23-SEP-1999; 99WO-US020881.
XX
PR 24-SEP-1998; 98US-0101594P.
XX
PA (PHAA) PHARMACIA & UPJOHN CO.
XX
PI Gurney ME, Bienkowski MJ, Heinrikson RL, Parodi LA, Yan R;
XX
DR WPI; 2000-303209/26.
DR P-PSDB; AAY88437.

XX
PT New enzyme designated human aspartase useful in research into Alzheimer's
PT Disease is capable of cleaving amyloid protein precursor at the beta
PT secretase site to produce amyloid beta peptide.
XX
PS Example 9; Page 165; 183pp; English.
XX
CC This sequence represents a modified version of the human aspartase 2
CC (Asp2) nucleotide sequence. The sequence is used in the bacterial
CC expression of human Asp2L. The invention relates to a protease (e.g.
CC Asp2) capable of cleaving the beta secretase site of amyloid precursor
CC protein (APP). The protease contains a sequence encoding the amino acid
CC sequence DTG and a sequence encoding DSG or DTG separated by 100-300
CC amino acids. When mutated the APP gene causes an autosomal dominant form
CC of Alzheimer's disease. APP localises to the cell surface membrane and
CC have a single C-terminal transmembrane domain. Proteolytic processing of
CC APP produces the amyloid beta protein, which is possibly very important
CC in Alzheimer's disease. The invention includes a nucleotide sequence
CC encoding the protease, a vector containing the nucleotide sequence, and a
CC cell line comprising the vector. Methods for screening for inhibitors of
CC beta secretase activity are also given in the invention. The human
CC aspartase protein and nucleotide sequences and the methods for
CC identifying inhibitors of the protease, are useful in the treatment of
CC and research in to Alzheimer's disease
XX
SQ Sequence 1278 BP; 284 A; 356 C; 353 G; 285 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	4.8e-14	Length:	1278
Score:	144.00	Matches:	28
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	3	Gaps:	0

US-10-726-967A-52 (1-28) x AAA15677 (1-1278)

```
Qy          1 GlyTyrTyrValGluMetThrValGlySerProProGlnThrLeuAsnIleLeuValAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGAT 195

Qy         21 ThrGlySerSerAsnPheAlaVal 28
              ||||||||||||||||||||||||||
Db        196 ACAGGCAGCAGTAACTTTGCAGTG 219
```

RESULT 2
AAS11714
ID AAS11714 standard; DNA; 1278 BP.
XX
AC AAS11714;
XX
DT 11-SEP-2003 (revised)
DT 24-OCT-2001 (first entry)
XX
DE DNA encoding T7-caspase-caspase 8-human aspartyl protease 2a deltaTM.
XX
KW Human; aspartyl protease 1; Asp-1; nootropic; neuroprotective;
KW aspartyl protease 2; Asp2; amyloid protein precursor; APP;
KW beta-secretase; Alzheimer's disease; ds.
XX
OS Homo sapiens.
OS Enterobacteria phage T7.
XX

FH	Key	Location/Qualifiers
FT	CDS	1. .1278
FT		/*tag= a
FT		/product= "T7-caspase-caspase 8-Aspartyl protease-2a
FT		delta TM"

XX
PN WO200149097-A2.
XX
PD 12-JUL-2001.
XX
PF 09-MAY-2001; 2001WO-IB000797.
XX
PR 09-MAY-2001; 2001WO-IB000797.
XX
PA (BIEN/) BIENKOWSKI M J.
PA (GURN/) GURNEY M E.
PA (HEIN/) HEINRIKSON R L.
PA (PARO/) PARODI L A.
PA (YANR/) YAN R.
XX
PI Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;
XX
DR WPI; 2001-502548/55.
DR P-PSDB; AAU07214.
XX
PT Novel purified polypeptide comprising fragment of mammalian aspartyl
PT protease 2, lacking Asp2 transmembrane domain and retaining beta
PT secretase activity of Asp2 useful for identifying inhibitors of Asp2
PT activity.
XX
PS Example 9; Page 158; 185pp; English.
XX
CC The invention relates to a novel purified polypeptide comprising a
CC fragment of mammalian aspartyl protease 2 (Asp2) protein which lacks the
CC Asp2 transmembrane domain and the Asp2 protein, and where the polypeptide
CC and the fragment retain the beta-secretase activity of the mammalian Asp2
CC protein. Also included is an isoform of amyloid protein precursor (APP)
CC comprising the amino acid sequence of a APP or its fragment containing an
CC APP cleavage site recognisable by a mammalian beta-secretase, and further
CC comprising two lysine residues at the carboxyl terminus of the amino acid
CC sequence of the mammalian APP or APP fragment. The polypeptides are used
CC for assaying for modulators of beta-secretase activity; identifying
CC agents that inhibit the APP processing activity of human Asp2 aspartyl
CC protease (Hu-Asp2); identifying agents that modulate the activity of Asp2
CC ; and for reducing cellular production of amyloid beta (Abeta) from APP.
CC Agents identified by the above methods are useful for treating
CC Alzheimer's disease; and for identifying modulators of amyloid-beta
CC (Abeta) peptide production, for use in designing therapeutics for the
CC treatment or prevention of Alzheimer's disease. Probes and primers
CC derived from Asp nucleic acid sequences are useful for detecting Hu-Asp
CC nucleic acids in in vitro assays and in Northern and Southern blots. The
CC present sequence represents the coding sequence of T7-caspase-caspase 8-
CC human-Asp-2a delta TM construct which has a T7 tag, a caspase 8 leader
CC sequence and cleavage site, and lacks the transmembrane domain. This
CC construct was used for bacterial expression and purification of human
CC Asp2a. (Updated on 11-SEP-2003 to standardise OS field)
XX
SQ Sequence 1278 BP; 284 A; 356 C; 353 G; 285 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	4.8e-14	Length:	1278
Score:	144.00	Matches:	28
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	4	Gaps:	0

US-10-726-967A-52 (1-28) x AAS11714 (1-1278)

```
Qy          1 GlyTyrTyrValGluMetThrValGlySerProProGlnThrLeuAsnIleLeuValAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGAT 195

Qy         21 ThrGlySerSerAsnPheAlaVal 28
              ||||||||||||||||||||||||||
Db        196 ACAGGCAGCAGTAACTTTGCAGTG 219
```

RESULT 3
AAD17877
ID AAD17877 standard; cDNA; 1278 BP.
XX
AC AAD17877;
XX

```
DT   10-DEC-2001  (first entry)
XX
DE   T7-Caspase-Caspase 8 cleavage-human-pro-Asp2(a) lacking TM domain cDNA.
XX
KW   Human; aspartyl protease 1; Asp1; amyloid precursor protein; APP;
KW   Alzheimer's disease; AD; dementia; neurofibrillary tangle; gliosis;
KW   amyloid plaque; neuronal loss; proteolytic; nootropic; neuroprotective;
KW   T7-Caspase-Caspase 8 cleavage-Human-pro-Asp 2(a) protein; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1278
FT                   /*tag=  a
FT                   /product= "T7-Caspase-Caspase 8 cleavage-Human-pro- Asp
FT                   2(a) protein lacking transmembrane domain"
XX
PN   GB2357767-A.
XX
PD   04-JUL-2001.
XX
PF   22-SEP-2000; 2000GB-00023315.
XX
PR   23-SEP-1999;   99US-00404133.
PR   23-SEP-1999;   99US-0155493P.
PR   23-SEP-1999;   99WO-US020881.
PR   13-OCT-1999;   99US-00416901.
PR   06-DEC-1999;   99US-0169232P.
XX
PA   (PHAA ) PHARMACIA & UPJOHN CO.
XX
PI   Bienkowkski MJ,  Gurney M;
XX
DR   WPI; 2001-444208/48.
DR   P-PSDB; AAE10641.
XX
PT   Polypeptide comprising fragments of human aspartyl protease with amyloid
PT   precursor protein processing activity and alpha-secretase activity, for
PT   identifying modulators useful in treating Alzheimer's disease.
XX
PS   Example 9; Page 128; 187pp; English.
XX
CC   The patent discloses human aspartyl protease 1 (hu-Asp1) or modified Asp1
CC   proteins which lack transmembrane domain or amino terminal domain or
CC   cytoplasmic domain and retains alpha-secretase activity and amyloid
CC   protein precursor (APP) processing activity. The proteins of the
CC   invention are useful for assaying hu-Asp1 alpha-secretase activity, which
CC   in turn is useful for identifying modulators of hu-Asp1 alpha-secretase
CC   activity, where modulators that increase hu-Asp1 alpha-secretase activity
CC   are useful for treating Alzheimer's disease (AD) which causes progressive
CC   dementia with consequent formation of amyloid plaques, neurofibrillary
CC   tangles, gliosis and neuronal loss. Hu-Asp1 protease substrate is useful
CC   for assaying hu-Asp1 proteolytic activity, by contacting hu-Asp1 protein
CC   with the substrate under acidic conditions and determining the level of
CC   hu-Asp1 proteolytic activity. The present sequence is a cDNA encoding T7-
CC   Caspase-Caspase 8 cleavage-human-pro-Asp 2(a) protein lacking a
CC   transmembrane (TM) domain which is generated from human Asp 2(a) protein
CC   by the addition of T7 tag and caspase 8 leader sequence at its N-terminal
CC   end and deletion of its C-terminal transmembrane domain
XX
SQ   Sequence 1278 BP; 284 A; 356 C; 353 G; 285 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              4.8e-14       Length:          1278
Score:                  144.00        Matches:         28
Percent Similarity:     100.00%       Conservative:    0
Best Local Similarity:  100.00%       Mismatches:      0
Query Match:            100.00%       Indels:          0
DB:                     4             Gaps:            0

US-10-726-967A-52 (1-28) x AAD17877 (1-1278)

Qy          1 GlyTyrTyrValGluMetThrValGlySerProProGlnThrLeuAsnIleLeuValAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGAT 195

Qy         21 ThrGlySerSerAsnPheAlaVal 28
              ||||||||||||||||||||||||
Db        196 ACAGGCAGCAGTAACTTTGCAGTG 219

RESULT 4
AAD13033
ID   AAD13033 standard; cDNA; 1278 BP.
XX
AC   AAD13033;
XX
DT   23-OCT-2001  (first entry)
XX
DE   T7-Caspase-Caspase 8 cleavage-Human-pro-Asp2(a) deltaTM protein cDNA.
XX
KW   Human; aspartyl protease 2a; Asp 2a; beta-amyloid precursor protein; APP;
KW   beta-secretase; Alzheimer's disease; dementia; amyloid plaque; gliosis;
KW   neurofibrillary tangle; neuronal loss; amyloid-beta peptide; nootropic;
KW   neuroprotective; antisense therapy; gene therapy;
KW   caspase-caspase 8 cleavage-pro-Asp2(a) deltaTM protein; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1278
FT                   /*tag=  a
FT                   /product= "T7-Caspase-Caspase 8 cleavage-Human-pro-
FT                   Asp2(a) deltaTM protein"
XX
PN   WO200150829-A2.
XX
PD   19-JUL-2001.
XX
PF   09-MAY-2001; 2001WO-IB000799.
XX
PR   09-MAY-2001; 2001WO-IB000799.
XX
PA   (BIEN/) BIENKOWSKI M J.
PA   (GURN/) GURNEY M E.
PA   (HEIN/) HEINRIKSON R L.
PA   (PARO/) PARODI L A.
PA   (YANR/) YAN R.
XX
PI   Bienkowski MJ,  Gurney ME,  Heinrikson RL,  Parodi LA,  Yan R;
XX
DR   WPI; 2001-483072/52.
DR   P-PSDB; AAE06871.
XX
PT   Novel purified polypeptide comprising fragment of mammalian aspartyl
PT   protease 2, lacking Asp2 transmembrane domain and retaining beta
PT   secretase activity of Asp2 useful for identifying inhibitors of Asp2
PT   activity.
XX
PS   Example 9; Page 158; 185pp; English.
XX
CC   The invention relates to human aspartyl proteases (Hu-Asp), beta-amyloid
CC   precursor protein (APP) isoforms and their corresponding DNA molecules.
CC   Human aspartyl proteases can act as beta-secretase proteases useful for
CC   treating Alzheimer's disease. APP isoforms are useful for identifying
CC   modulators of amyloid-beta peptide production, for use in designing
CC   therapeutics for the treatment and prevention of Alzheimer's disease,
CC   dementia, formation of amyloid plaques, neurofibrillary tangles, gliosis
CC   and neuronal loss. APP isoforms are also used in methods for identifying
CC   inhibitors and modulators of human Asp2 activity. The invention relates
CC   to a method for identifying agents that modulate the activity of human
CC   aspartyl protease Asp2. Amyloid-beta peptides obtained from APP are used
CC   as a means to screen in cellular assays for the inhibitors of beta- and
CC   gamma- secretase. Hu-Asp DNA fragments are useful as probes or primers in
CC   polymerase chain reactions (PCR). The probes are useful for detecting Hu-
```

```
CC   Asp nucleic acids in in vitro assays and in Northern and Southern blots.
CC   The present cDNA sequence encodes T7-Caspase-Caspase 8 cleavage- Human-
CC   pro-aspartyl protease 2a (Asp2a) deltaTM protein which is obtained by the
CC   addition of T7 tag and caspase 8 leader sequence at the N-terminal end
CC   and deletion of the transmembrane domain at the C-terminal end of Hu-
CC   Asp2a. Human Asp2a has beta-secretase activity
XX
SQ   Sequence 1278 BP; 284 A; 356 C; 353 G; 285 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                4.8e-14       Length:          1278
Score:                    144.00        Matches:         28
Percent Similarity:       100.00%       Conservative:    0
Best Local Similarity:    100.00%       Mismatches:      0
Query Match:              100.00%       Indels:          0
DB:                       4             Gaps:            0

US-10-726-967A-52 (1-28) x AAD13033 (1-1278)

Qy          1 GlyTyrTyrValGluMetThrValGlySerProProGlnThrLeuAsnIleLeuValAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGAT 195

Qy         21 ThrGlySerSerAsnPheAlaVal 28
              |||||||||||||||||||||||||
Db        196 ACAGGCAGCAGTAACTTTGCAGTG 219

RESULT 5
AAD06751
ID   AAD06751 standard; cDNA; 1278 BP.
XX
AC   AAD06751;
XX
DT   10-AUG-2001  (first entry)
XX
DE   T7-Caspase-Caspase 8-cleavage-human-pro-Asp-2(a) delta TM protein cDNA.
XX
KW   Human; alpha-secretase; amyloid precursor protein; APP; therapy;
KW   Alzheimer's disease; antialzheimer's; aspartyl protease 2a; Asp2a;
KW   beta-secretase; caspase-caspase 8-Asp-2a delta TM; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1278
FT                   /*tag=  a
FT                   /product= "T7-Caspase-Caspase 8-cleavage-human-pro- Asp-
FT                   2(a) delta TM protein"
XX
PN   WO200123533-A2.
XX
PD   05-APR-2001.
XX
PF   22-SEP-2000; 2000WO-US026080.
XX
PR   23-SEP-1999;   99US-0155493P.
PR   23-SEP-1999;   99WO-US020881.
PR   13-OCT-1999;   99US-00416901.
PR   06-DEC-1999;   99US-0169232P.
XX
PA   (PHAA ) PHARMACIA & UPJOHN CO.
XX
PI   Gurney M,  Bienkowski MJ;
XX
DR   WPI; 2001-290516/30.
DR   P-PSDB; AAE02593.
XX
PT   Enzymes that cleave the alpha-secretase site of the amyloid precursor
PT   protein, useful for the treatment of Alzheimer's disease.
XX
PS   Example 9; Page 157; 189pp; English.
XX
CC   The present invention relates to enzymes for cleaving the alpha-
CC   secretase site of the amyloid precursor protein (APP) and methods of
CC   identifying those enzymes. The methods may be used to identify enzymes
CC   that may be used to cleave the alpha-secretase cleavage site of the APP
CC   protein. The enzymes may be used to treat or modulate the progress of
CC   Alzheimer's disease. The present sequence is a cDNA encoding human
CC   Aspartyl protease 2a (Asp-2a) caspase-caspase 8-deltaTM protein which is
CC   obtained by deleting the transmembrane domain and adding a T7-caspase
CC   leader sequence at the N-terminal end. This sequence has beta-secretase
CC   protease activity
XX
SQ   Sequence 1278 BP; 284 A; 356 C; 353 G; 285 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                4.8e-14       Length:          1278
Score:                    144.00        Matches:         28
Percent Similarity:       100.00%       Conservative:    0
Best Local Similarity:    100.00%       Mismatches:      0
Query Match:              100.00%       Indels:          0
DB:                       4             Gaps:            0

US-10-726-967A-52 (1-28) x AAD06751 (1-1278)

Qy          1 GlyTyrTyrValGluMetThrValGlySerProProGlnThrLeuAsnIleLeuValAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGAT 195

Qy         21 ThrGlySerSerAsnPheAlaVal 28
              |||||||||||||||||||||||||
Db        196 ACAGGCAGCAGTAACTTTGCAGTG 219

RESULT 6
AAS11529
ID   AAS11529 standard; cDNA; 1278 BP.
XX
AC   AAS11529;
XX
DT   24-OCT-2001  (first entry)
XX
DE   T7-Caspase-caspase-8-Human-pro-Asp 2(a) delta TM fusion protein cDNA.
XX
KW   Human; Aspartyl protease; beta-secretase; nootropic; ASP2;
KW   neuroprotective; amyloid protein precursor; APP; Alzheimer's disease;
KW   amyloid-beta; Abeta; T7-Caspase-caspase 8-Human-pro-Asp 2(a) delta TM;
KW   ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1278
FT                   /*tag=  a
FT                   /product= "T7-Caspase-caspase 8-Human-pro-Asp 2(a) delta
FT                   TM fusion protein"
FT   sig_peptide     43. .87
FT                   /*tag=  b
FT                   /note= "Caspase leader sequence"
FT   mat_peptide     88. .1275
FT                   /label= Mature_Asp_2(a)
FT                   /note= "Also encodes 5 extra N-terminal amino acids
FT                   constituting a caspase 8 cleavage site"
XX
PN   WO200149098-A2.
XX
PD   12-JUL-2001.
XX
PF   09-MAY-2001; 2001WO-IB000798.
XX
PR   09-MAY-2001; 2001WO-IB000798.
XX
PA   (BIEN/) BIENKOWSKI M J.
PA   (GURN/) GURNEY M E.
PA   (HEIN/) HEINRIKSON R L.
```

PA (PARO/) PARODI L A.
PA (YANR/) YAN R.
XX
PI Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;
XX
DR WPI; 2001-502549/55.
DR P-PSDB; AAU06615.
XX
PT Novel purified polypeptide comprising fragment of mammalian aspartyl
PT protease 2, lacking Asp2 transmembrane domain and retaining beta
PT secretase activity of Asp2 useful for identifying inhibitors of Asp2
PT activity.
XX
PS Example 9; Page 158; 185pp; English.
XX
CC The invention relates to a purified polypeptide comprising a fragment of
CC mammalian aspartyl protease (Asp)2 protein which lacks the Asp2
CC transmembrane domain and the Asp2 protein, and where the polypeptide and
CC the fragment retain the beta-secretase activity of the mammalian Asp2
CC protein. The invention also details polynucleotides for the Asp proteins
CC and vectors expressing them, and a polypeptide (isoform of amyloid
CC protein precursor (APP)) comprising the amino acid sequence of an APP or
CC its fragment containing an APP cleavage site recognizable by a mammalian
CC beta-secretase, and further comprising two lysine residues at the
CC carboxyl terminus of the amino acid sequence of the mammalian APP or APP
CC fragment. Also included in the invention are methods of identifying
CC modulators or inhibitors of Asp2. Modulators and inhibitors of Asp2 are
CC useful for treating Alzheimer's disease. APP is useful in methods for
CC identifying inhibitors or modulators of human Asp2 activity and amyloid-
CC beta (Abeta) peptide production. APP is also useful in designing
CC therapeutics for the treatment or prevention of Alzheimer's disease. APP
CC comprising the APP-Sw-beta-secretase peptide sequence (NLDA), which is
CC associated with increased levels of Abeta processing is useful in assays
CC relating the Alzheimer's research. The expression vector is useful for
CC recombinantly expressing APP. Nucleic acids that hybridise to Asp
CC oligonucleotides are useful as probes or primers. The probes are useful
CC for detecting Hu-Asp nucleic acids in in vitro assays and in Northern and
CC Southern blots. The present sequence encodes T7-Caspase- caspase 8-Human-
CC pro-Asp 2(a) delta TM fusion protein which has a N-terminal T7 tag to aid
CC purification when expressed in E. coli, a Caspase leader sequence and a
CC caspase 8 cleavage signal to aid cleavage of the signal peptide
XX
SQ Sequence 1278 BP; 284 A; 356 C; 353 G; 285 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	4.8e-14	Length:	1278
Score:	144.00	Matches:	28
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	4	Gaps:	0

US-10-726-967A-52 (1-28) x AAS11529 (1-1278)

```
Qy          1 GlyTyrTyrValGluMetThrValGlySerProProGlnThrLeuAsnIleLeuValAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGAT 195

Qy         21 ThrGlySerSerAsnPheAlaVal 28
              |||||||||||||||||||||||||
Db        196 ACAGGCAGCAGTAACTTTGCAGTG 219
```

RESULT 7
ABL52469
ID ABL52469 standard; cDNA; 1278 BP.
XX
AC ABL52469;
XX
DT 16-JUL-2002 (first entry)
XX
DE T7-caspase-caspase 8 cleavage-human-pro-Asp-2(a)deltaTM nucleotide.
XX
KW Human; Asp-1; Asp-2; aspartyl protease; Alzheimer's disease; proteolytic;
KW amyloid precursor protein; APP; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1. .1278
FT /*tag= a
FT /product= "T7-caspase-caspase 8 cleavage-human-pro- Asp-
FT 2(a)deltaTM"
XX
PN GB2367060-A.
XX
PD 27-MAR-2002.
XX
PF 29-OCT-2001; 2001GB-00025934.
XX
PR 23-SEP-1999; 99US-00404133.
PR 23-SEP-1999; 99US-0155493P.
PR 23-SEP-1999; 99WO-US020881.
PR 13-OCT-1999; 99US-00416901.
PR 06-DEC-1999; 99US-0169232P.
PR 22-SEP-2000; 2000GB-00023315.
XX
PA (PHAA) PHARMACIA & UPJOHN CO.
XX
PI Bienkowkski MJ, Gurney M;
XX
DR WPI; 2002-397167/43.
DR P-PSDB; ABB78602.
XX
PT Human aspartyl protease 1 substrates useful in assays to detect aspartyl
PT protease activity, e.g. for the diagnosis of Alzheimer's disease.
XX
PS Example 9; Page 128; 182pp; English.
XX
CC The present invention describes a human aspartyl protease 1 (hu-Asp1)
CC substrate (I) which comprises a peptide of no more than 50 amino acids,
CC and which comprises the 8 amino acid sequence Gly-Leu-Ala-Leu-Ala-Leu-
CC Glu-Pro. Also described are: (1) a method (II) for assaying hu-Asp1
CC proteolytic activity, comprising: (a) contacting a hu-Asp1 protein with
CC (I) under acidic conditions; and (b) determining the level of hu-Asp1
CC proteolytic activity; (2) a purified polynucleotide (III) comprising a
CC nucleotide sequence that hybridises under stringent conditions to the non
CC -coding strand complementary to a defined 1804 nucleotide sequence (see
CC ABL52456) where the nucleotide sequence encodes a polypeptide having Asp1
CC proteolytic activity and lacks nucleotides encoding a transmembrane
CC domain); (3) a purified polynucleotide (III') comprising a sequence that
CC hybridises under stringent conditions to (III) (the nucleotide sequence
CC encodes a polypeptide further lacking a pro-peptide domain corresponding
CC to amino acids 23-62 of hu-Asp1 (see ABB78589)); (4) a vector (IV)
CC comprising (III) or (III'); and (5) a host cell (V) transformed or
CC transfected with (III), (III') and/or (IV). The hu-Asp1 protease
CC substrate (I) may be used as an enzyme substrate in assays to detect
CC aspartyl protease activity, (II) and therefore diagnose diseases
CC associated with aberrant hu-Asp1 expression and activity such as
CC Alzheimer's disease. Hu-Asp1 has been localised to chromosome 21, while
CC hu-Asp2 has been localised to chromosome 11q23.3-24.1. The present
CC sequence encodes T7-caspase-caspase 8 cleavage-human-pro-Asp-2(a)deltaTM,
CC which is given in an example from the present invention
XX
SQ Sequence 1278 BP; 284 A; 356 C; 353 G; 285 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	4.8e-14	Length:	1278
Score:	144.00	Matches:	28
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0

US-10-726-967A-52 (1-28) x ABL52469 (1-1278)

```
Qy          1 GlyTyrTyrValGluMetThrValGlySerProProGlnThrLeuAsnIleLeuValAsp 20
```

```
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGAT 195

Qy         21 ThrGlySerSerAsnPheAlaVal 28
                ||||||||||||||||||||||||
Db        196 ACAGGCAGCAGTAACTTTGCAGTG 219

RESULT 8
ADJ94339
ID   ADJ94339 standard; cDNA; 1278 BP.
XX
AC   ADJ94339;
XX
DT   03-JUN-2004  (first entry)
XX
DE   Human T7-Caspase-Caspase 8 cleavage-human-pro-Asp-2(a)deltaTM cDNA.
XX
KW   Human; ss; gene; aspartyl protease; Asp-1; Asp-2(a); Asp-2(b);
KW   beta secretase; amyloid protein precursor; APP; Alzheimer's disease;
KW   nootropic; neuroprotective; amyloid beta; mutant.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   US6706485-B1.
XX
PD   16-MAR-2004.
XX
PF   12-APR-2000; 2000US-00548376.
XX
PR   24-SEP-1998;   98US-0101594P.
PR   23-SEP-1999;   99US-00404133.
PR   23-SEP-1999;   99US-0155493P.
PR   23-SEP-1999;   99WO-US020881.
PR   13-OCT-1999;   99US-00416901.
XX
PA   (PHAA ) PHARMACIA & UPJOHN CO.
XX
PI   Gurney ME,  Bienkowski MJ,  Heinrikson RL,  Parodi LA,  Yan R;
XX
DR   WPI; 2004-236722/22.
DR   P-PSDB; ADJ94340.
XX
PT   Identifying agents that modulate activity of Asp2 aspartyl protease
PT   useful for treating or preventing Alzheimer's disease involves comparing
PT   APP processing activity of protease in presence and absence of test
PT   agent.
XX
PS   Disclosure; SEQ ID NO 27; 109pp; English.
XX
CC   The invention relates to identifying agents that modulate activity of
CC   Asp2 (e.g. a beta-secretase, e.g. human Asp-2(b) appearing as ID 6,
CC   encoded by ID 5) aspartyl protease, involves contacting Asp2 with amyloid
CC   precursor protein (APP) in the presence and absence of a test agent,
CC   where Asp2 is a recombinant polypeptide and processes APP into amyloid
CC   beta, determining APP processing activity of Asp2 in presence and absence
CC   of the test agent, and comparing the activities to identify agents that
CC   modulate the activity of Asp2. Also disclosed are the cDNA and proteins
CC   for human Asp-1 and Asp-2(a), mouse Asp-2(b), a vector comprising the
CC   nucleic acid encoding Hu-Asp2 protease sequence, a host cell comprising
CC   the vector and the method of producing Hu-Asp polypeptide, an isolated
CC   antibody that specifically binds to Hu-Asp polypeptides, identifying a
CC   cell that can be used to screen for inhibitors of beta secretase
CC   activity, novel isoforms of amyloid protein precursor (APP), where the
CC   last 2 carboxy terminus amino acids of that isoform are both lysine
CC   residues (e.g. those designated APP695-KK or carrying the Swedish
CC   mutation where KM at 595-596 is mutated to NL, designated e.g. APP695-Sw
CC   or APP695-Sw-KK, or a V to F mutation at 642, e.g. APP695-VF, all useful
CC   for assaying for beta secretase activity and screening for inhibitors of
CC   beta-secretase) and polynucleotides that encode the APP proteins. The
CC   method is useful for identifying agents that modulate the activity
CC   (amyloid precursor protein processing activity) of Asp2 aspartyl
CC   protease. Preferably, the method is useful for identifying agents that
CC   inhibit Asp2 aspartyl protease activity. The inhibitors of amyloid
CC   precursor protein processing, are useful for treating or preventing
CC   Alzheimer's disease. The present sequence encodes an aspartyl protease
CC   mutant construct (e.g. lacking a transmembrane domain and/or including a
CC   caspase cleavage site) used to investigate the cleavage activity of Asp2
CC   proteins.
XX
SQ   Sequence 1278 BP; 284 A; 356 C; 353 G; 285 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                4.8e-14        Length:          1278
Score:                    144.00         Matches:         28
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              100.00%        Indels:          0
DB:                       12             Gaps:            0

US-10-726-967A-52 (1-28) x ADJ94339 (1-1278)

Qy          1 GlyTyrTyrValGluMetThrValGlySerProProGlnThrLeuAsnIleLeuValAsp 20
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGAT 195

Qy         21 ThrGlySerSerAsnPheAlaVal 28
                ||||||||||||||||||||||||
Db        196 ACAGGCAGCAGTAACTTTGCAGTG 219

RESULT 9
ADO50435
ID   ADO50435 standard; DNA; 1278 BP.
XX
AC   ADO50435;
XX
DT   29-JUL-2004  (first entry)
XX
DE   T7-Caspase-Caspase 8 cleavage-Human-pro-Asp-2(a)deltaTM DNA.
XX
KW   Aspartyl protease; Asp; beta secretase; amyloid precursor protein; APP;
KW   Alzheimer's disease; gene therapy; caspase; human; gene; chimeric; ds.
XX
OS   Homo sapiens.
OS   Chimeric.
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1278
FT                   /*tag=  a
FT                   /product= "T7-Caspase-Caspase 8 cleavage-Human-pro-Asp-
FT                   2(a)deltaTM protein"
XX
PN   US6737510-B1.
XX
PD   18-MAY-2004.
XX
PF   12-APR-2000; 2000US-00548373.
XX
PR   24-SEP-1998;   98US-0101594P.
PR   23-SEP-1999;   99US-00404133.
PR   23-SEP-1999;   99US-0155493P.
PR   23-SEP-1999;   99WO-US020881.
PR   13-OCT-1999;   99US-00416901.
XX
PA   (PHAA ) PHARMACIA & UPJOHN CO.
XX
PI   Gurney ME,  Bienkowski MJ,  Heinrikson RL,  Parodi LA,  Yan R;
XX
DR   WPI; 2004-387112/36.
DR   P-PSDB; ADO50436.
XX
PT   New Asp2 aspartyl protease protein comprising tripeptides DTG and DSG
PT   involved in processing amyloid precursor protein into amyloid beta,
PT   useful in preparing a composition for treating or preventing Alzheimer's
PT   disease.
```

```
XX
PS   Example 9; SEQ ID NO 27; 108pp; English.
XX
CC   The invention relates to a method for identifying an agent that decreases
CC   the protease activity of the aspartyl protease (Asp) polypeptide. It also
CC   provides enzyme and enzymatic procedures for cleaving the beta secretase
CC   cleavage site of the amyloid precursor protein (APP). The invention is
CC   useful in preparing a composition for treating or preventing Alzheimer's
CC   disease. It is also useful in gene therapy. The present sequence is T7-
CC   Caspase-Caspase 8 cleavage-Human-pro-Asp-2(a)deltaTM chimeric DNA. This
CC   sequence is used to illustrate the method of the invention.
XX
SQ   Sequence 1278 BP; 284 A; 356 C; 353 G; 285 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                4.8e-14        Length:          1278
Score:                    144.00         Matches:         28
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              100.00%        Indels:          0
DB:                       12             Gaps:            0

US-10-726-967A-52 (1-28) x ADO50435 (1-1278)

Qy          1 GlyTyrTyrValGluMetThrValGlySerProProGlnThrLeuAsnIleLeuValAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGAT 195

Qy         21 ThrGlySerSerAsnPheAlaVal 28
              |||||||||||||||||||||||||
Db        196 ACAGGCAGCAGTAACTTTGCAGTG 219

RESULT 10
ADR75348
ID   ADR75348 standard; DNA; 1278 BP.
XX
AC   ADR75348;
XX
DT   18-NOV-2004  (first entry)
XX
DE   T7-Caspase-Caspase 8 cleavage-Human-pro-Asp-2(a)deltaTM DNA.
XX
KW   Aspartyl protease; Asp; amyloid precursor protein; APP; amyloid beta;
KW   chromosome identification; Alzheimer's disease; human; caspase; chimeric;
KW   gene; ds.
XX
OS   Homo sapiens.
OS   Chimeric.
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1278
FT                   /*tag=  a
FT                   /product= "T7-Caspase-Caspase 8 cleavage-Human-pro-Asp-
FT                   2(a)deltaTM protein"
XX
PN   US2004166507-A1.
XX
PD   26-AUG-2004.
XX
PF   29-AUG-2003; 2003US-00652045.
XX
PR   24-SEP-1998;   98US-0101594P.
PR   23-SEP-1999;   99US-00404133.
PR   23-SEP-1999;   99US-0155493P.
PR   13-OCT-1999;   99US-00416901.
XX
PA   (GURN/) GURNEY M E.
PA   (BIEN/) BIENKOWAKI M J.
PA   (HEIN/) HEINRIKSON R L.
PA   (PARO/) PARODI L A.
PA   (YANR/) YAN R.
XX
PI   Gurney ME,  Bienkowaki MJ,  Heinrikson RL,  Parodi LA,  Yan R;
XX
DR   WPI; 2004-624916/60.
DR   P-PSDB; ADR75349.
XX
PT   Novel purified/isolated polynucleotide encoding polypeptide having
PT   aspartyl protease activity involved in processing amyloid precursor
PT   protein into amyloid beta, useful in identifying agent decreasing
PT   activity of aspartyl protease.
XX
PS   Example 9; SEQ ID NO 27; 107pp; English.
XX
CC   The invention relates to nucleic acid sequences encoding aspartyl
CC   protease (Asp) polypeptides having aspartyl protease activity involved in
CC   processing amyloid precursor protein (APP) into amyloid beta. The
CC   invention also relates to a method for identifying an agent that
CC   decreases the protease activity of the Asp. Asp DNA is useful in
CC   chromosome identification as they can hybridise with a specific location
CC   on a human chromosome and in identifying the relationship between genes
CC   and diseases (particular gene responsible for causing diseases). It is
CC   also useful for identifying candidates to modulate the progression of
CC   Alzheimer's disease. Asp is useful in raising antibodies that are useful
CC   in diagnostic assay for detecting Hu-Asp polypeptide expression. The
CC   present sequence is the T7-Caspase-Caspase 8 cleavage-Human-pro-Asp-
CC   2(a)deltaTM DNA. This sequence is used to illustrate the method of the
CC   invention.
XX
SQ   Sequence 1278 BP; 284 A; 356 C; 353 G; 285 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                4.8e-14        Length:          1278
Score:                    144.00         Matches:         28
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              100.00%        Indels:          0
DB:                       13             Gaps:            0

US-10-726-967A-52 (1-28) x ADR75348 (1-1278)

Qy          1 GlyTyrTyrValGluMetThrValGlySerProProGlnThrLeuAsnIleLeuValAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGAT 195

Qy         21 ThrGlySerSerAsnPheAlaVal 28
              |||||||||||||||||||||||||
Db        196 ACAGGCAGCAGTAACTTTGCAGTG 219

RESULT 11
AAD17895
ID   AAD17895 standard; cDNA; 1287 BP.
XX
AC   AAD17895;
XX
DT   10-DEC-2001  (first entry)
XX
DE   Human-Asp 2(b) protein lacking transmembrane domain encoding cDNA.
XX
KW   Human; aspartyl protease 2b; Asp2b; amyloid precursor protein; APP;
KW   Alzheimer's disease; AD; dementia; neurofibrillary tangle; gliosis;
KW   amyloid plaque; neuronal loss; proteolytic; nootropic; neuroprotective;
KW   ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1287
FT                   /*tag=  a
FT                   /product= "Human-Asp 2(b) protein lacking transmembrane
FT                   domain"
XX
PN   GB2357767-A.
XX
```

```
PD   04-JUL-2001.
XX
PF   22-SEP-2000; 2000GB-00023315.
XX
PR   23-SEP-1999;   99US-00404133.
PR   23-SEP-1999;   99US-0155493P.
PR   23-SEP-1999;   99WO-US020881.
PR   13-OCT-1999;   99US-00416901.
PR   06-DEC-1999;   99US-0169232P.
XX
PA   (PHAA ) PHARMACIA & UPJOHN CO.
XX
PI   Bienkowkski MJ,  Gurney M;
XX
DR   WPI; 2001-444208/48.
DR   P-PSDB; AAE10646.
XX
PT   Polypeptide comprising fragments of human aspartyl protease with amyloid
PT   precursor protein processing activity and alpha-secretase activity, for
PT   identifying modulators useful in treating Alzheimer's disease.
XX
PS   Example 10; Page 137; 187pp; English.
XX
CC   The patent discloses human aspartyl protease 1 (hu-Asp1) or modified Asp1
CC   proteins which lack transmembrane domain or amino terminal domain or
CC   cytoplasmic domain and retains alpha-secretase activity and amyloid
CC   protein precursor (APP) processing activity. The proteins of the
CC   invention are useful for assaying hu-Asp1 alpha-secretase activity, which
CC   in turn is useful for identifying modulators of hu-Asp1 alpha-secretase
CC   activity, where modulators that increase hu-Asp1 alpha-secretase activity
CC   are useful for treating Alzheimer's disease (AD) which causes progressive
CC   dementia with consequent formation of amyloid plaques, neurofibrillary
CC   tangles, gliosis and neuronal loss. Hu-Asp1 protease substrate is useful
CC   for assaying hu-Asp1 proteolytic activity, by contacting hu-Asp1 protein
CC   with the substrate under acidic conditions and determining the level of
CC   hu-Asp1 proteolytic activity. The present sequence is a cDNA encoding
CC   human Asp 2(b) protein lacking a transmembrane (TM) domain which is
CC   generated by the deletion of the C-terminal TM domain and intracellular
CC   domains of human Asp 2(b) protein
XX
SQ   Sequence 1287 BP; 271 A; 370 C; 384 G; 262 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                4.84e-14      Length:          1287
Score:                    144.00        Matches:         28
Percent Similarity:       100.00%       Conservative:    0
Best Local Similarity:    100.00%       Mismatches:      0
Query Match:              100.00%       Indels:          0
DB:                       4             Gaps:            0

US-10-726-967A-52 (1-28) x AAD17895 (1-1287)

Qy          1 GlyTyrTyrValGluMetThrValGlySerProProGlnThrLeuAsnIleLeuValAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        220 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGAT 279

Qy         21 ThrGlySerSerAsnPheAlaVal 28
              ||||||||||||||||||||||||||
Db        280 ACAGGCAGCAGTAACTTTGCAGTG 303

RESULT 12
AAD13276
ID   AAD13276 standard; cDNA; 1287 BP.
XX
AC   AAD13276;
XX
DT   23-OCT-2001  (first entry)
XX
DE   Human-Asp2(b) deltaTM protein cDNA.
XX
KW   Human; aspartyl protease 2b; Asp 2b; beta-amyloid precursor protein; APP;
KW   beta-secretase; Alzheimer's disease; dementia; amyloid plaque; gliosis;
KW   neurofibrillary tangle; neuronal loss; amyloid-beta peptide; nootropic;
KW   neuroprotective; antisense therapy; Asp2(b) deltaTM protein;
KW   gene therapy; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1287
FT                   /*tag=  a
FT                   /product= "Human Asp2(b) deltaTM protein"
XX
PN   WO200150829-A2.
XX
PD   19-JUL-2001.
XX
PF   09-MAY-2001; 2001WO-IB000799.
XX
PR   09-MAY-2001; 2001WO-IB000799.
XX
PA   (BIEN/) BIENKOWSKI M J.
PA   (GURN/) GURNEY M E.
PA   (HEIN/) HEINRIKSON R L.
PA   (PARO/) PARODI L A.
PA   (YANR/) YAN R.
XX
PI   Bienkowski MJ,  Gurney ME,  Heinrikson RL,  Parodi LA,  Yan R;
XX
DR   WPI; 2001-483072/52.
DR   P-PSDB; AAE06891.
XX
PT   Novel purified polypeptide comprising fragment of mammalian aspartyl
PT   protease 2, lacking Asp2 transmembrane domain and retaining beta
PT   secretase activity of Asp2 useful for identifying inhibitors of Asp2
PT   activity.
XX
PS   Example 10; Page 166-167; 185pp; English.
XX
CC   The invention relates to human aspartyl proteases (Hu-Asp), beta-amyloid
CC   precursor protein (APP) isoforms and their corresponding DNA molecules.
CC   Human aspartyl proteases can act as beta-secretase proteases useful for
CC   treating Alzheimer's disease. APP isoforms are useful for identifying
CC   modulators of amyloid-beta peptide production, for use in designing
CC   therapeutics for the treatment and prevention of Alzheimer's disease,
CC   dementia, formation of amyloid plaques, neurofibrillary tangles, gliosis
CC   and neuronal loss. APP isoforms are also used in methods for identifying
CC   inhibitors and modulators of human Asp2 activity. The invention relates
CC   to a method for identifying agents that modulate the activity of human
CC   aspartyl protease Asp2. Amyloid-beta peptides obtained from APP are used
CC   as a means to screen in cellular assays for the inhibitors of beta- and
CC   gamma- secretase. Hu-Asp DNA fragments are useful as probes or primers in
CC   polymerase chain reactions (PCR). The probes are useful for detecting Hu-
CC   Asp nucleic acids in in vitro assays and in Northern and Southern blots.
CC   The present cDNA sequence encodes Human aspartyl protease 2b (Hu-Asp2b)
CC   deltaTM protein which is obtained by the deletion of C-terminal
CC   transmembrane and intracellular domains of Hu-Asp2b. Human Asp2b has beta
CC   -secretase activity
XX
SQ   Sequence 1287 BP; 271 A; 370 C; 384 G; 262 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                4.84e-14      Length:          1287
Score:                    144.00        Matches:         28
Percent Similarity:       100.00%       Conservative:    0
Best Local Similarity:    100.00%       Mismatches:      0
Query Match:              100.00%       Indels:          0
DB:                       4             Gaps:            0

US-10-726-967A-52 (1-28) x AAD13276 (1-1287)

Qy          1 GlyTyrTyrValGluMetThrValGlySerProProGlnThrLeuAsnIleLeuValAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        220 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGAT 279
```

```
Qy         21 ThrGlySerSerAsnPheAlaVal 28
              ||||||||||||||||||||||||
Db        280 ACAGGCAGCAGTAACTTTGCAGTG 303

RESULT 13
AAD06768
ID   AAD06768 standard; cDNA; 1287 BP.
XX
AC   AAD06768;
XX
DT   10-AUG-2001  (first entry)
XX
DE   Human aspartyl protease 2 (b) delta TM cDNA.
XX
KW   Human; alpha-secretase; amyloid precursor protein; APP; therapy;
KW   Alzheimer's disease; antialzheimer's; aspartyl protease 2; Asp 2;
KW   beta-secretase; chromosome 11q23.3-24.1; mutant; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1287
FT                   /*tag=  a
FT                   /product= "Human aspartyl protease 2 (b) delta TM"
XX
PN   WO200123533-A2.
XX
PD   05-APR-2001.
XX
PF   22-SEP-2000; 2000WO-US026080.
XX
PR   23-SEP-1999;   99US-0155493P.
PR   23-SEP-1999;   99WO-US020881.
PR   13-OCT-1999;   99US-00416901.
PR   06-DEC-1999;   99US-0169232P.
XX
PA   (PHAA ) PHARMACIA & UPJOHN CO.
XX
PI   Gurney M,  Bienkowski MJ;
XX
DR   WPI; 2001-290516/30.
DR   P-PSDB; AAE02598.
XX
PT   Enzymes that cleave the alpha-secretase site of the amyloid precursor
PT   protein, useful for the treatment of Alzheimer's disease.
XX
PS   Example 10; Page 165-166; 189pp; English.
XX
CC   The present invention relates to enzymes for cleaving the alpha-
CC   secretase site of the amyloid precursor protein (APP) and methods of
CC   identifying those enzymes. The methods may be used to identify enzymes
CC   that may be used to cleave the alpha-secretase cleavage site of the APP
CC   protein. The enzymes may be used to treat or modulate the progress of
CC   Alzheimer's disease. The present sequence is human aspartyl protease 2
CC   (Asp 2) (b) delta TM cDNA. The Asp 2 gene from which it is derived is
CC   located on chromosome 11q23.3-24.1. The Asp 2 has beta-secretase protease
CC   activity
XX
SQ   Sequence 1287 BP; 271 A; 370 C; 384 G; 262 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                4.84e-14        Length:          1287
Score:                    144.00          Matches:         28
Percent Similarity:       100.00%         Conservative:    0
Best Local Similarity:    100.00%         Mismatches:      0
Query Match:              100.00%         Indels:          0
DB:                       4               Gaps:            0

US-10-726-967A-52 (1-28) x AAD06768 (1-1287)

Qy          1 GlyTyrTyrValGluMetThrValGlySerProProGlnThrLeuAsnIleLeuValAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        220 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGAT 279

Qy         21 ThrGlySerSerAsnPheAlaVal 28
              ||||||||||||||||||||||||
Db        280 ACAGGCAGCAGTAACTTTGCAGTG 303

RESULT 14
AAS11547
ID   AAS11547 standard; cDNA; 1287 BP.
XX
AC   AAS11547;
XX
DT   24-OCT-2001  (first entry)
XX
DE   Human cDNA encoding Human-pro-Asp 2(b) delta TM.
XX
KW   Human; Aspartyl protease; beta-secretase; nootropic; ASP2;
KW   neuroprotective; amyloid protein precursor; APP; Alzheimer's disease;
KW   amyloid-beta; Abeta; Human-pro-Asp 2(b) delta TM; ss; mutant.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1287
FT                   /*tag=  a
FT                   /product= "Human-pro-Asp 2(b) delta TM"
XX
PN   WO200149098-A2.
XX
PD   12-JUL-2001.
XX
PF   09-MAY-2001; 2001WO-IB000798.
XX
PR   09-MAY-2001; 2001WO-IB000798.
XX
PA   (BIEN/) BIENKOWSKI M J.
PA   (GURN/) GURNEY M E.
PA   (HEIN/) HEINRIKSON R L.
PA   (PARO/) PARODI L A.
PA   (YANR/) YAN R.
XX
PI   Bienkowski MJ,  Gurney ME,  Heinrikson RL,  Parodi LA,  Yan R;
XX
DR   WPI; 2001-502549/55.
XX
PT   Novel purified polypeptide comprising fragment of mammalian aspartyl
PT   protease 2, lacking Asp2 transmembrane domain and retaining beta
PT   secretase activity of Asp2 useful for identifying inhibitors of Asp2
PT   activity.
XX
PS   Disclosure; Page 166-167; 185pp; English.
XX
CC   The invention relates to a purified polypeptide comprising a fragment of
CC   mammalian aspartyl protease (Asp)2 protein which lacks the Asp2
CC   transmembrane domain and the Asp2 protein, and where the polypeptide and
CC   the fragment retain the beta-secretase activity of the mammalian Asp2
CC   protein. The invention also details polynucleotides for the Asp proteins
CC   and vectors expressing them, and a polypeptide (isoform of amyloid
CC   protein precursor (APP)) comprising the amino acid sequence of an APP or
CC   its fragment containing an APP cleavage site recognizable by a mammalian
CC   beta-secretase, and further comprising two lysine residues at the
CC   carboxyl terminus of the amino acid sequence of the mammalian APP or APP
CC   fragment. Also included in the invention are methods of identifying
CC   modulators or inhibitors of Asp2. Modulators and inhibitors of Asp2 are
CC   useful for treating Alzheimer's disease. APP is useful in methods for
CC   identifying inhibitors or modulators of human Asp2 activity and amyloid-
CC   beta (Abeta) peptide production. APP is also useful in designing
CC   therapeutics for the treatment or prevention of Alzheimer's disease. APP
CC   comprising the APP-Sw-beta-secretase peptide sequence (NLDA), which is
CC   associated with increased levels of Abeta processing is useful in assays
CC   relating the Alzheimer's research. The expression vector is useful for
CC   recombinantly expressing APP. Nucleic acids that hybridise to Asp
```

```
CC   oligonucleotides are useful as probes or primers. The probes are useful
CC   for detecting Hu-Asp nucleic acids in in vitro assays and in Northern and
CC   Southern blots. The present sequence encodes Human-pro- Asp 2(b) delta TM
CC   protein, which lacks the C-terminal transmembrane domain
XX
SQ   Sequence 1287 BP; 271 A; 370 C; 384 G; 262 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              4.84e-14       Length:         1287
Score:                  144.00         Matches:        28
Percent Similarity:     100.00%        Conservative:   0
Best Local Similarity:  100.00%        Mismatches:     0
Query Match:            100.00%        Indels:         0
DB:                     4              Gaps:           0

US-10-726-967A-52 (1-28) x AAS11547 (1-1287)

Qy          1 GlyTyrTyrValGluMetThrValGlySerProProGlnThrLeuAsnIleLeuValAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        220 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGAT 279

Qy         21 ThrGlySerSerAsnPheAlaVal 28
              ||||||||||||||||||||||||
Db        280 ACAGGCAGCAGTAACTTTGCAGTG 303

RESULT 15
ABL52487
ID   ABL52487 standard; cDNA; 1287 BP.
XX
AC   ABL52487;
XX
DT   16-JUL-2002  (first entry)
XX
DE   Human Asp-2(b)deltaTM nucleotide sequence SEQ ID NO:50.
XX
KW   Human; Asp-1; Asp-2; aspartyl protease; Alzheimer's disease; proteolytic;
KW   chromosome 11q23.3-24.1; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1287
FT                   /*tag= a
FT                   /product= "Human Asp-2(b)delta TM"
XX
PN   GB2367060-A.
XX
PD   27-MAR-2002.
XX
PF   29-OCT-2001; 2001GB-00025934.
XX
PR   23-SEP-1999;   99US-00404133.
PR   23-SEP-1999;   99US-0155493P.
PR   23-SEP-1999;   99WO-US020881.
PR   13-OCT-1999;   99US-00416901.
PR   06-DEC-1999;   99US-0169232P.
PR   22-SEP-2000; 2000GB-00023315.
XX
PA   (PHAA ) PHARMACIA & UPJOHN CO.
XX
PI   Bienkowkski MJ,  Gurney M;
XX
DR   WPI; 2002-397167/43.
DR   P-PSDB; ABB78607.
XX
PT   Human aspartyl protease 1 substrates useful in assays to detect aspartyl
PT   protease activity, e.g. for the diagnosis of Alzheimer's disease.
XX
PS   Example 10; Page 137; 182pp; English.
XX
CC   The present invention describes a human aspartyl protease 1 (hu-Asp1)
CC   substrate (I) which comprises a peptide of no more than 50 amino acids,
CC   and which comprises the 8 amino acid sequence Gly-Leu-Ala-Leu-Ala-Leu-
CC   Glu-Pro. Also described are: (1) a method (II) for assaying hu-Asp1
CC   proteolytic activity, comprising: (a) contacting a hu-Asp1 protein with
CC   (I) under acidic conditions; and (b) determining the level of hu-Asp1
CC   proteolytic activity; (2) a purified polynucleotide (III) comprising a
CC   nucleotide sequence that hybridises under stringent conditions to the non
CC   -coding strand complementary to a defined 1804 nucleotide sequence (see
CC   ABL52456) where the nucleotide sequence encodes a polypeptide having Asp1
CC   proteolytic activity and lacks nucleotides encoding a transmembrane
CC   domain); (3) a purified polynucleotide (III') comprising a sequence that
CC   hybridises under stringent conditions to (III) (the nucleotide sequence
CC   encodes a polypeptide further lacking a pro-peptide domain corresponding
CC   to amino acids 23-62 of hu-Asp1 (see ABB78589)); (4) a vector (IV)
CC   comprising (III) or (III'); and (5) a host cell (V) transformed or
CC   transfected with (III), (III') and/or (IV). The hu-Asp1 protease
CC   substrate (I) may be used as an enzyme substrate in assays to detect
CC   aspartyl protease activity, (II) and therefore diagnose diseases
CC   associated with aberrant hu-Asp1 expression and activity such as
CC   Alzheimer's disease. Hu-Asp1 has been localised to chromosome 21, while
CC   hu-Asp2 has been localised to chromosome 11q23.3-24.1. The present
CC   sequence encodes human Asp-2(b)deltaTM, which is given in an example from
CC   the present invention
XX
SQ   Sequence 1287 BP; 271 A; 370 C; 384 G; 262 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              4.84e-14       Length:         1287
Score:                  144.00         Matches:        28
Percent Similarity:     100.00%        Conservative:   0
Best Local Similarity:  100.00%        Mismatches:     0
Query Match:            100.00%        Indels:         0
DB:                     6              Gaps:           0

US-10-726-967A-52 (1-28) x ABL52487 (1-1287)

Qy          1 GlyTyrTyrValGluMetThrValGlySerProProGlnThrLeuAsnIleLeuValAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        220 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGAT 279

Qy         21 ThrGlySerSerAsnPheAlaVal 28
              ||||||||||||||||||||||||
Db        280 ACAGGCAGCAGTAACTTTGCAGTG 303


Search completed: July 27, 2005, 17:25:06
Job time : 440 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: July 27, 2005, 16:49:48 ; Search time 132 Seconds
(without alignments)
347.089 Million cell updates/sec

Title: US-10-726-967A-52
Perfect score: 144
Sequence: 1 GYYVEMTVGSPPQTLNILVDTGSSNFAV 28

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US10726967/runat_26072005_130735_6165/app_query.fasta_1.199
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10726967_@CGN_1_1_105_@runat_26072005_130735_6165 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	144	100.0	1278	3	US-09-548-372D-27	Sequence 27, Appl
2	144	100.0	1278	3	US-09-548-367D-27	Sequence 27, Appl
3	144	100.0	1278	4	US-09-551-853D-27	Sequence 27, Appl
4	144	100.0	1278	4	US-09-416-901B-27	Sequence 27, Appl
5	144	100.0	1278	4	US-09-548-376D-27	Sequence 27, Appl
6	144	100.0	1278	4	US-09-794-927A-27	Sequence 27, Appl
7	144	100.0	1278	4	US-09-548-373D-27	Sequence 27, Appl
8	144	100.0	1278	4	US-09-795-847B-27	Sequence 27, Appl
9	144	100.0	1278	4	US-09-869-414-27	Sequence 27, Appl
10	144	100.0	1278	4	US-09-548-366F-27	Sequence 27, Appl
11	144	100.0	1278	4	US-09-548-368D-27	Sequence 27, Appl
12	144	100.0	1278	4	US-09-794-925A-27	Sequence 27, Appl
13	144	100.0	1278	4	US-09-806-194A-27	Sequence 27, Appl
14	144	100.0	1287	3	US-09-548-372D-50	Sequence 50, Appl
15	144	100.0	1287	3	US-09-548-367D-50	Sequence 50, Appl
16	144	100.0	1287	4	US-09-551-853D-50	Sequence 50, Appl
17	144	100.0	1287	4	US-09-416-901B-50	Sequence 50, Appl
18	144	100.0	1287	4	US-09-548-376D-50	Sequence 50, Appl
19	144	100.0	1287	4	US-09-794-927A-50	Sequence 50, Appl
20	144	100.0	1287	4	US-09-548-373D-50	Sequence 50, Appl
21	144	100.0	1287	4	US-09-795-847B-50	Sequence 50, Appl
22	144	100.0	1287	4	US-09-869-414-50	Sequence 50, Appl
23	144	100.0	1287	4	US-09-548-366F-50	Sequence 50, Appl
24	144	100.0	1287	4	US-09-548-368D-50	Sequence 50, Appl
25	144	100.0	1287	4	US-09-794-925A-50	Sequence 50, Appl
26	144	100.0	1302	3	US-09-548-372D-25	Sequence 25, Appl
27	144	100.0	1302	3	US-09-548-367D-25	Sequence 25, Appl
28	144	100.0	1302	4	US-09-551-853D-25	Sequence 25, Appl
29	144	100.0	1302	4	US-09-416-901B-25	Sequence 25, Appl
30	144	100.0	1302	4	US-09-548-376D-25	Sequence 25, Appl
31	144	100.0	1302	4	US-09-794-927A-25	Sequence 25, Appl
32	144	100.0	1302	4	US-09-548-373D-25	Sequence 25, Appl
33	144	100.0	1302	4	US-09-795-847B-25	Sequence 25, Appl
34	144	100.0	1302	4	US-09-869-414-25	Sequence 25, Appl
35	144	100.0	1302	4	US-09-548-366F-25	Sequence 25, Appl
36	144	100.0	1302	4	US-09-548-368D-25	Sequence 25, Appl
37	144	100.0	1302	4	US-09-794-925A-25	Sequence 25, Appl
38	144	100.0	1302	4	US-09-806-194A-25	Sequence 25, Appl
39	144	100.0	1305	3	US-09-548-372D-52	Sequence 52, Appl
40	144	100.0	1305	3	US-09-548-367D-52	Sequence 52, Appl
41	144	100.0	1305	4	US-09-551-853D-52	Sequence 52, Appl
42	144	100.0	1305	4	US-09-416-901B-52	Sequence 52, Appl
43	144	100.0	1305	4	US-09-548-376D-52	Sequence 52, Appl
44	144	100.0	1305	4	US-09-794-927A-52	Sequence 52, Appl
45	144	100.0	1305	4	US-09-548-373D-52	Sequence 52, Appl

ALIGNMENTS

RESULT 1
US-09-548-372D-27
; Sequence 27, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280I
; CURRENT APPLICATION NUMBER: US/09/548,372D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 1278
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-548-372D-27

Alignment Scores:

Pred. No.:	4.05e-16	Length:	1278
Score:	144.00	Matches:	28
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	3	Gaps:	0

US-10-726-967A-52 (1-28) x US-09-548-372D-27 (1-1278)

```
Qy          1 GlyTyrTyrValGluMetThrValGlySerProProGlnThrLeuAsnIleLeuValAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGAT 195

Qy         21 ThrGlySerSerAsnPheAlaVal 28
              |||||||||||||||||||||||||
Db        196 ACAGGCAGCAGTAACTTTGCAGTG 219

RESULT 2
US-09-548-367D-27
; Sequence 27, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
;  APPLICANT: GURNEY ET AL.
;  TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 29915/6280H
;  CURRENT APPLICATION NUMBER: US/09/548,367D
;  CURRENT FILING DATE:  2000-04-12
;  PRIOR APPLICATION NUMBER: US 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
;   LENGTH: 1278
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-548-367D-27

Alignment Scores:
Pred. No.:                4.05e-16        Length:         1278
Score:                    144.00          Matches:        28
Percent Similarity:       100.00%         Conservative:   0
Best Local Similarity:    100.00%         Mismatches:     0
Query Match:              100.00%         Indels:         0
DB:                       3               Gaps:           0

US-10-726-967A-52 (1-28) x US-09-548-367D-27 (1-1278)

Qy          1 GlyTyrTyrValGluMetThrValGlySerProProGlnThrLeuAsnIleLeuValAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGAT 195

Qy         21 ThrGlySerSerAsnPheAlaVal 28
              |||||||||||||||||||||||||
Db        196 ACAGGCAGCAGTAACTTTGCAGTG 219

RESULT 3
US-09-551-853D-27
; Sequence 27, Application US/09551853D
; Patent No. 6500667
; GENERAL INFORMATION:
;  APPLICANT: GURNEY ET AL.
;  TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 29915/6280L
;  CURRENT APPLICATION NUMBER: US/09/551,853D
;  CURRENT FILING DATE:  2000-04-18
;  PRIOR APPLICATION NUMBER: US 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
;   LENGTH: 1278
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-551-853D-27

Alignment Scores:
Pred. No.:                4.05e-16        Length:         1278
Score:                    144.00          Matches:        28
Percent Similarity:       100.00%         Conservative:   0
Best Local Similarity:    100.00%         Mismatches:     0
Query Match:              100.00%         Indels:         0
DB:                       4               Gaps:           0

US-10-726-967A-52 (1-28) x US-09-551-853D-27 (1-1278)

Qy          1 GlyTyrTyrValGluMetThrValGlySerProProGlnThrLeuAsnIleLeuValAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGAT 195

Qy         21 ThrGlySerSerAsnPheAlaVal 28
              |||||||||||||||||||||||||
Db        196 ACAGGCAGCAGTAACTTTGCAGTG 219

RESULT 4
US-09-416-901B-27
; Sequence 27, Application US/09416901B
; Patent No. 6699671
; GENERAL INFORMATION:
;  APPLICANT: GURNEY ET AL.
;  TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 29915/6280A
;  CURRENT APPLICATION NUMBER: US/09/416,901B
;  CURRENT FILING DATE:  1999-10-13
;  PRIOR APPLICATION NUMBER: US 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 72
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
;   LENGTH: 1278
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-416-901B-27

Alignment Scores:
Pred. No.:                4.05e-16        Length:         1278
Score:                    144.00          Matches:        28
Percent Similarity:       100.00%         Conservative:   0
Best Local Similarity:    100.00%         Mismatches:     0
Query Match:              100.00%         Indels:         0
DB:                       4               Gaps:           0

US-10-726-967A-52 (1-28) x US-09-416-901B-27 (1-1278)

Qy          1 GlyTyrTyrValGluMetThrValGlySerProProGlnThrLeuAsnIleLeuValAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGAT 195

Qy         21 ThrGlySerSerAsnPheAlaVal 28
              |||||||||||||||||||||||||
Db        196 ACAGGCAGCAGTAACTTTGCAGTG 219

RESULT 5
US-09-548-376D-27
```

```
; Sequence 27, Application US/09548376D
; Patent No. 6706485
; GENERAL INFORMATION:
;  APPLICANT: GURNEY ET AL.
;  TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR
;  TITLE OF INVENTION:  AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 29915/6280F
;  CURRENT APPLICATION NUMBER: US/09/548,376D
;  CURRENT FILING DATE:  2000-04-12
;  PRIOR APPLICATION NUMBER: US 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
;   LENGTH: 1278
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-548-376D-27

Alignment Scores:
Pred. No.:                4.05e-16      Length:          1278
Score:                    144.00        Matches:         28
Percent Similarity:       100.00%       Conservative:    0
Best Local Similarity:    100.00%       Mismatches:      0
Query Match:              100.00%       Indels:          0
DB:                       4             Gaps:            0

US-10-726-967A-52 (1-28) x US-09-548-376D-27 (1-1278)

Qy          1 GlyTyrTyrValGluMetThrValGlySerProProGlnThrLeuAsnIleLeuValAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGAT 195

Qy         21 ThrGlySerSerAsnPheAlaVal 28
              |||||||||||||||||||||||||
Db        196 ACAGGCAGCAGTAACTTTGCAGTG 219

RESULT 6
US-09-794-927A-27
; Sequence 27, Application US/09794927A
; Patent No. 6727074
; GENERAL INFORMATION:
;  APPLICANT: Gurney et al.
;  TITLE OF INVENTION: Alzheimer's Disease Secretase, APP Substrates Therefor and Uses
;  TITLE OF INVENTION:  Therefor
;  FILE REFERENCE: 29915/6280FG
;  CURRENT APPLICATION NUMBER: US/09/794,927A
;  CURRENT FILING DATE:  2001-02-27
;  PRIOR APPLICATION NUMBER: 09/416,901
;  PRIOR FILING DATE: 1999-10-13
;  PRIOR APPLICATION NUMBER: 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 74
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
;   LENGTH: 1278
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-794-927A-27

Alignment Scores:
Pred. No.:                4.05e-16      Length:          1278
Score:                    144.00        Matches:         28
Percent Similarity:       100.00%       Conservative:    0
Best Local Similarity:    100.00%       Mismatches:      0
Query Match:              100.00%       Indels:          0
DB:                       4             Gaps:            0

US-10-726-967A-52 (1-28) x US-09-794-927A-27 (1-1278)

Qy          1 GlyTyrTyrValGluMetThrValGlySerProProGlnThrLeuAsnIleLeuValAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGAT 195

Qy         21 ThrGlySerSerAsnPheAlaVal 28
              |||||||||||||||||||||||||
Db        196 ACAGGCAGCAGTAACTTTGCAGTG 219

RESULT 7
US-09-548-373D-27
; Sequence 27, Application US/09548373D
; Patent No. 6737510
; GENERAL INFORMATION:
;  APPLICANT: GURNEY ET AL.
;  TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 29915/6280B
;  CURRENT APPLICATION NUMBER: US/09/548,373D
;  CURRENT FILING DATE:  2000-04-12
;  PRIOR APPLICATION NUMBER: US 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
;   LENGTH: 1278
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-548-373D-27

Alignment Scores:
Pred. No.:                4.05e-16      Length:          1278
Score:                    144.00        Matches:         28
Percent Similarity:       100.00%       Conservative:    0
Best Local Similarity:    100.00%       Mismatches:      0
Query Match:              100.00%       Indels:          0
DB:                       4             Gaps:            0

US-10-726-967A-52 (1-28) x US-09-548-373D-27 (1-1278)

Qy          1 GlyTyrTyrValGluMetThrValGlySerProProGlnThrLeuAsnIleLeuValAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGAT 195

Qy         21 ThrGlySerSerAsnPheAlaVal 28
              |||||||||||||||||||||||||
Db        196 ACAGGCAGCAGTAACTTTGCAGTG 219

RESULT 8
US-09-795-847B-27
; Sequence 27, Application US/09795847B
; Patent No. 6753163
; GENERAL INFORMATION:
;  APPLICANT: Gurney, Mark E.
;  APPLICANT:  Bienkowski, Michael J.
;  APPLICANT:  Heinrikson, Robert L.
;  APPLICANT:  Parodi, Luis A.
;  APPLICANT:  Yan, Riqiang
```

```
;  TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE: 28341/6280DE
;  CURRENT APPLICATION NUMBER: US/09/795,847B
;  CURRENT FILING DATE:  2001-02-28
;  PRIOR APPLICATION NUMBER: 09/416,901
;  PRIOR FILING DATE: 1999-10-13
;  PRIOR APPLICATION NUMBER: 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 74
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
;   LENGTH: 1278
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-795-847B-27

Alignment Scores:
Pred. No.:                4.05e-16        Length:         1278
Score:                    144.00          Matches:        28
Percent Similarity:       100.00%         Conservative:   0
Best Local Similarity:    100.00%         Mismatches:     0
Query Match:              100.00%         Indels:         0
DB:                       4               Gaps:           0

US-10-726-967A-52 (1-28) x US-09-795-847B-27 (1-1278)

Qy          1 GlyTyrTyrValGluMetThrValGlySerProProGlnThrLeuAsnIleLeuValAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGAT 195

Qy         21 ThrGlySerSerAsnPheAlaVal 28
              ||||||||||||||||||||||||||
Db        196 ACAGGCAGCAGTAACTTTGCAGTG 219

RESULT 9
US-09-869-414-27
; Sequence 27, Application US/09869414
; Patent No. 6790610
; GENERAL INFORMATION:
;  APPLICANT: Beinkowski et al.
;  TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE: 28341/6280M
;  CURRENT APPLICATION NUMBER: US/09/869,414
;  CURRENT FILING DATE:  2001-06-27
;  PRIOR APPLICATION NUMBER: 09/416,901
;  PRIOR FILING DATE: 1999-10-13
;  PRIOR APPLICATION NUMBER: 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
;   LENGTH: 1278
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-869-414-27

Alignment Scores:
Pred. No.:                4.05e-16        Length:         1278
Score:                    144.00          Matches:        28
Percent Similarity:       100.00%         Conservative:   0
Best Local Similarity:    100.00%         Mismatches:     0
Query Match:              100.00%         Indels:         0
DB:                       4               Gaps:           0

US-10-726-967A-52 (1-28) x US-09-869-414-27 (1-1278)

Qy          1 GlyTyrTyrValGluMetThrValGlySerProProGlnThrLeuAsnIleLeuValAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGAT 195

Qy         21 ThrGlySerSerAsnPheAlaVal 28
              ||||||||||||||||||||||||||
Db        196 ACAGGCAGCAGTAACTTTGCAGTG 219

RESULT 10
US-09-548-366F-27
; Sequence 27, Application US/09548366F
; Patent No. 6797487
; GENERAL INFORMATION:
;  APPLICANT: GURNEY ET AL.
;  TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 29915/6280J
;  CURRENT APPLICATION NUMBER: US/09/548,366F
;  CURRENT FILING DATE:  2000-04-12
;  PRIOR APPLICATION NUMBER: US 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
;   LENGTH: 1278
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-548-366F-27

Alignment Scores:
Pred. No.:                4.05e-16        Length:         1278
Score:                    144.00          Matches:        28
Percent Similarity:       100.00%         Conservative:   0
Best Local Similarity:    100.00%         Mismatches:     0
Query Match:              100.00%         Indels:         0
DB:                       4               Gaps:           0

US-10-726-967A-52 (1-28) x US-09-548-366F-27 (1-1278)

Qy          1 GlyTyrTyrValGluMetThrValGlySerProProGlnThrLeuAsnIleLeuValAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGAT 195

Qy         21 ThrGlySerSerAsnPheAlaVal 28
              ||||||||||||||||||||||||||
Db        196 ACAGGCAGCAGTAACTTTGCAGTG 219

RESULT 11
US-09-548-368D-27
; Sequence 27, Application US/09548368D
; Patent No. 6825023
; GENERAL INFORMATION:
;  APPLICANT: GURNEY ET AL.
;  TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 29915/6280C
;  CURRENT APPLICATION NUMBER: US/09/548,368D
;  CURRENT FILING DATE:  2000-04-12
;  PRIOR APPLICATION NUMBER: US 60/155,493
;  PRIOR FILING DATE: 1999-09-23
```

```
;  PRIOR APPLICATION NUMBER: US 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
;   LENGTH: 1278
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-548-368D-27

Alignment Scores:
Pred. No.:                4.05e-16        Length:         1278
Score:                    144.00          Matches:        28
Percent Similarity:       100.00%         Conservative:   0
Best Local Similarity:    100.00%         Mismatches:     0
Query Match:              100.00%         Indels:         0
DB:                       4               Gaps:           0

US-10-726-967A-52 (1-28) x US-09-548-368D-27 (1-1278)

Qy          1 GlyTyrTyrValGluMetThrValGlySerProProGlnThrLeuAsnIleLeuValAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGAT 195

Qy         21 ThrGlySerSerAsnPheAlaVal 28
              ||||||||||||||||||||||||||
Db        196 ACAGGCAGCAGTAACTTTGCAGTG 219

RESULT 12
US-09-794-925A-27
; Sequence 27, Application US/09794925A
; Patent No. 6828117
; GENERAL INFORMATION:
;  APPLICANT: Gurney et al.
;  TITLE OF INVENTION: Alzheimer's Disease Secretase, APP Substrates Therefor and Uses
;  TITLE OF INVENTION:  Therefor
;  FILE REFERENCE: 29915/6280HI
;  CURRENT APPLICATION NUMBER: US/09/794,925A
;  CURRENT FILING DATE:  2001-02-27
;  PRIOR APPLICATION NUMBER: 09/416,901
;  PRIOR FILING DATE: 1999-10-13
;  PRIOR APPLICATION NUMBER: 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 74
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
;   LENGTH: 1278
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-794-925A-27

Alignment Scores:
Pred. No.:                4.05e-16        Length:         1278
Score:                    144.00          Matches:        28
Percent Similarity:       100.00%         Conservative:   0
Best Local Similarity:    100.00%         Mismatches:     0
Query Match:              100.00%         Indels:         0
DB:                       4               Gaps:           0

US-10-726-967A-52 (1-28) x US-09-794-925A-27 (1-1278)

Qy          1 GlyTyrTyrValGluMetThrValGlySerProProGlnThrLeuAsnIleLeuValAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGAT 195

Qy         21 ThrGlySerSerAsnPheAlaVal 28
              ||||||||||||||||||||||||||
Db        196 ACAGGCAGCAGTAACTTTGCAGTG 219

RESULT 13
US-09-806-194A-27
; Sequence 27, Application US/09806194A
; Patent No. 6835565
; GENERAL INFORMATION:
;  APPLICANT: Gurney, Mark E.
;  APPLICANT:  Bienkowski, Michael J.
;  APPLICANT:  Heinrikson, Robert L.
;  APPLICANT:  Parodi, Luis A.
;  APPLICANT:  Yan, Riqiang
;  APPLICANT:  Pharmacia & Upjohn Company
;  TITLE OF INVENTION: Alzheimer's Disease Secretase
;  FILE REFERENCE: 6177.P CP
;  CURRENT APPLICATION NUMBER: US/09/806,194A
;  CURRENT FILING DATE:  2001-09-17
;  PRIOR APPLICATION NUMBER: 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 49
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
;   LENGTH: 1278
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-806-194A-27

Alignment Scores:
Pred. No.:                4.05e-16        Length:         1278
Score:                    144.00          Matches:        28
Percent Similarity:       100.00%         Conservative:   0
Best Local Similarity:    100.00%         Mismatches:     0
Query Match:              100.00%         Indels:         0
DB:                       4               Gaps:           0

US-10-726-967A-52 (1-28) x US-09-806-194A-27 (1-1278)

Qy          1 GlyTyrTyrValGluMetThrValGlySerProProGlnThrLeuAsnIleLeuValAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGAT 195

Qy         21 ThrGlySerSerAsnPheAlaVal 28
              ||||||||||||||||||||||||||
Db        196 ACAGGCAGCAGTAACTTTGCAGTG 219

RESULT 14
US-09-548-372D-50
; Sequence 50, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
;  APPLICANT: GURNEY ET AL.
;  TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 29915/6280I
;  CURRENT APPLICATION NUMBER: US/09/548,372D
;  CURRENT FILING DATE:  2000-04-12
;  PRIOR APPLICATION NUMBER: US 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 50
;   LENGTH: 1287
;   TYPE: DNA
```

```
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Hu-Asp2(b) delta TM
US-09-548-372D-50

Alignment Scores:
Pred. No.:              4.09e-16        Length:         1287
Score:                  144.00          Matches:        28
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     3               Gaps:           0

US-10-726-967A-52 (1-28) x US-09-548-372D-50 (1-1287)

Qy          1 GlyTyrTyrValGluMetThrValGlySerProProGlnThrLeuAsnIleLeuValAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        220 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGAT 279

Qy         21 ThrGlySerSerAsnPheAlaVal 28
              |||||||||||||||||||||||||
Db        280 ACAGGCAGCAGTAACTTTGCAGTG 303

RESULT 15
US-09-548-367D-50
; Sequence 50, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
;  APPLICANT: GURNEY ET AL.
;  TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 29915/6280H
;  CURRENT APPLICATION NUMBER: US/09/548,367D
;  CURRENT FILING DATE:  2000-04-12
;  PRIOR APPLICATION NUMBER: US 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 50
;   LENGTH: 1287
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Hu-Asp2(b) delta TM
US-09-548-367D-50

Alignment Scores:
Pred. No.:              4.09e-16        Length:         1287
Score:                  144.00          Matches:        28
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     3               Gaps:           0

US-10-726-967A-52 (1-28) x US-09-548-367D-50 (1-1287)

Qy          1 GlyTyrTyrValGluMetThrValGlySerProProGlnThrLeuAsnIleLeuValAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        220 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGAT 279

Qy         21 ThrGlySerSerAsnPheAlaVal 28
              |||||||||||||||||||||||||
Db        280 ACAGGCAGCAGTAACTTTGCAGTG 303


Search completed: July 27, 2005, 18:52:41
Job time : 134 secs
```

GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: July 27, 2005, 17:18:01 ; Search time 627 Seconds
(without alignments)
288.765 Million cell updates/sec

Title: US-10-726-967A-52
Perfect score: 144
Sequence: 1 GYYVEMTVGSPPQTLNILVDTGSSNFAV 28

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 7277826 seqs, 3233139505 residues

Total number of hits satisfying chosen parameters: 14555652

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US10726967/runat_26072005_130735_6188/app_query.fasta_1.199
-DB=Published_Applications_NA -QFMT=fastap -SUFFIX=p2n.rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US10726967_@CGN_1_1_723_@runat_26072005_130735_6188
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
19: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq:*
20: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq:*
21: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq:*
22: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
23: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq:*
24: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
25: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	144	100.0	1278	9	US-09-794-927-27	Sequence 27, Appl
2	144	100.0	1278	9	US-09-795-847-27	Sequence 27, Appl
3	144	100.0	1278	9	US-09-794-743-27	Sequence 27, Appl
4	144	100.0	1278	9	US-09-794-748-27	Sequence 27, Appl
5	144	100.0	1278	9	US-09-794-925-27	Sequence 27, Appl
6	144	100.0	1278	9	US-09-681-442-27	Sequence 27, Appl
7	144	100.0	1278	10	US-09-869-414-27	Sequence 27, Appl
8	144	100.0	1278	10	US-09-548-366-27	Sequence 27, Appl
9	144	100.0	1278	18	US-10-652-927-27	Sequence 27, Appl
10	144	100.0	1278	18	US-10-652-830-27	Sequence 27, Appl
11	144	100.0	1278	19	US-10-652-045-27	Sequence 27, Appl
12	144	100.0	1278	20	US-10-476-935-27	Sequence 27, Appl
13	144	100.0	1278	21	US-10-940-867-27	Sequence 27, Appl
14	144	100.0	1278	21	US-10-477-076-27	Sequence 27, Appl
15	144	100.0	1287	9	US-09-794-927-50	Sequence 50, Appl
16	144	100.0	1287	9	US-09-795-847-50	Sequence 50, Appl
17	144	100.0	1287	9	US-09-794-743-50	Sequence 50, Appl
18	144	100.0	1287	9	US-09-794-748-50	Sequence 50, Appl
19	144	100.0	1287	9	US-09-794-925-50	Sequence 50, Appl
20	144	100.0	1287	9	US-09-681-442-50	Sequence 50, Appl
21	144	100.0	1287	10	US-09-869-414-50	Sequence 50, Appl
22	144	100.0	1287	10	US-09-548-366-50	Sequence 50, Appl
23	144	100.0	1287	18	US-10-652-927-50	Sequence 50, Appl
24	144	100.0	1287	18	US-10-652-830-50	Sequence 50, Appl
25	144	100.0	1287	19	US-10-652-045-50	Sequence 50, Appl
26	144	100.0	1287	20	US-10-476-935-50	Sequence 50, Appl
27	144	100.0	1287	21	US-10-477-076-50	Sequence 50, Appl
28	144	100.0	1302	9	US-09-794-927-25	Sequence 25, Appl
29	144	100.0	1302	9	US-09-795-847-25	Sequence 25, Appl
30	144	100.0	1302	9	US-09-794-743-25	Sequence 25, Appl
31	144	100.0	1302	9	US-09-794-748-25	Sequence 25, Appl
32	144	100.0	1302	9	US-09-794-925-25	Sequence 25, Appl
33	144	100.0	1302	9	US-09-681-442-25	Sequence 25, Appl
34	144	100.0	1302	10	US-09-869-414-25	Sequence 25, Appl
35	144	100.0	1302	10	US-09-548-366-25	Sequence 25, Appl
36	144	100.0	1302	18	US-10-652-927-25	Sequence 25, Appl
37	144	100.0	1302	18	US-10-652-830-25	Sequence 25, Appl
38	144	100.0	1302	19	US-10-652-045-25	Sequence 25, Appl
39	144	100.0	1302	20	US-10-476-935-25	Sequence 25, Appl
40	144	100.0	1302	21	US-10-940-867-25	Sequence 25, Appl
41	144	100.0	1302	21	US-10-477-076-25	Sequence 25, Appl
42	144	100.0	1305	9	US-09-794-927-52	Sequence 52, Appl
43	144	100.0	1305	9	US-09-795-847-52	Sequence 52, Appl
44	144	100.0	1305	9	US-09-794-743-52	Sequence 52, Appl
45	144	100.0	1305	9	US-09-794-748-52	Sequence 52, Appl

ALIGNMENTS

RESULT 1
US-09-794-927-27
; Sequence 27, Application US/09794927
; Patent No. US20010016324A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280FG
; CURRENT APPLICATION NUMBER: US/09/794,927
; CURRENT FILING DATE: 2001-02-27

```
;  PRIOR APPLICATION NUMBER:  09/416,901
;  PRIOR FILING DATE:  1999-10-13
;  PRIOR APPLICATION NUMBER:  60/155,493
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  09/404,133
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  PCT/US99/20881
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  60/101,594
;  PRIOR FILING DATE:  1998-09-24
;  NUMBER OF SEQ ID NOS:  73
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 27
;   LENGTH: 1278
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-794-927-27

Alignment Scores:
Pred. No.:                2.82e-14       Length:          1278
Score:                    144.00         Matches:         28
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              100.00%        Indels:          0
DB:                       9              Gaps:            0

US-10-726-967A-52 (1-28) x US-09-794-927-27 (1-1278)

Qy          1 GlyTyrTyrValGluMetThrValGlySerProProGlnThrLeuAsnIleLeuValAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGAT 195

Qy         21 ThrGlySerSerAsnPheAlaVal 28
              ||||||||||||||||||||||||||
Db        196 ACAGGCAGCAGTAACTTTGCAGTG 219

RESULT 2
US-09-795-847-27
; Sequence 27, Application US/09795847
; Patent No. US20010018208A1
; GENERAL INFORMATION:
;  APPLICANT:  Gurney, Mark E.
;  APPLICANT:  Bienkowski, Michael J.
;  APPLICANT:  Heinrikson, Robert L.
;  APPLICANT:  Parodi, Luis A.
;  APPLICANT:  Yan, Riqiang
;  TITLE OF INVENTION:  ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
;  TITLE OF INVENTION:  USES
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE:  28341/6280DE
;  CURRENT APPLICATION NUMBER: US/09/795,847
;  CURRENT FILING DATE:  2001-02-28
;  PRIOR APPLICATION NUMBER:  09/416,901
;  PRIOR FILING DATE:  1999-10-13
;  PRIOR APPLICATION NUMBER:  60/155,493
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  09/404,133
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  PCT/US99/20881
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  60/101,594
;  PRIOR FILING DATE:  1998-09-24
;  NUMBER OF SEQ ID NOS:  73
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 27
;   LENGTH: 1278
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-795-847-27

Alignment Scores:
Pred. No.:                2.82e-14       Length:          1278
Score:                    144.00         Matches:         28
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              100.00%        Indels:          0
DB:                       9              Gaps:            0

US-10-726-967A-52 (1-28) x US-09-795-847-27 (1-1278)

Qy          1 GlyTyrTyrValGluMetThrValGlySerProProGlnThrLeuAsnIleLeuValAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGAT 195

Qy         21 ThrGlySerSerAsnPheAlaVal 28
              ||||||||||||||||||||||||||
Db        196 ACAGGCAGCAGTAACTTTGCAGTG 219

RESULT 3
US-09-794-743-27
; Sequence 27, Application US/09794743
; Patent No. US20010021391A1
; GENERAL INFORMATION:
;  APPLICANT:  Gurney, Mark E.
;  APPLICANT:  Bienkowski, Michael J.
;  APPLICANT:  Heinrikson, Robert L.
;  APPLICANT:  Parodi, Luis A.
;  APPLICANT:  Yan, Riqiang
;  TITLE OF INVENTION:  ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
;  TITLE OF INVENTION:  USES
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE:  28341/6280BC
;  CURRENT APPLICATION NUMBER: US/09/794,743
;  CURRENT FILING DATE:  2001-02-27
;  PRIOR APPLICATION NUMBER:  09/416,901
;  PRIOR FILING DATE:  1999-10-13
;  PRIOR APPLICATION NUMBER:  60/155,493
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  09/404,133
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  PCT/US99/20881
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  60/101,594
;  PRIOR FILING DATE:  1998-09-24
;  NUMBER OF SEQ ID NOS:  73
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 27
;   LENGTH: 1278
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-794-743-27

Alignment Scores:
Pred. No.:                2.82e-14       Length:          1278
Score:                    144.00         Matches:         28
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              100.00%        Indels:          0
DB:                       9              Gaps:            0

US-10-726-967A-52 (1-28) x US-09-794-743-27 (1-1278)

Qy          1 GlyTyrTyrValGluMetThrValGlySerProProGlnThrLeuAsnIleLeuValAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGAT 195

Qy         21 ThrGlySerSerAsnPheAlaVal 28
              ||||||||||||||||||||||||||
Db        196 ACAGGCAGCAGTAACTTTGCAGTG 219

RESULT 4
US-09-794-748-27
; Sequence 27, Application US/09794748
; Patent No. US20020037315A1
; GENERAL INFORMATION:
;  APPLICANT:  Gurney, Mark E.
```

```
;  APPLICANT:  Bienkowski, Michael J.
;  APPLICANT:  Heinrikson, Robert L.
;  APPLICANT:  Parodi, Luis A.
;  APPLICANT:  Yan, Riqiang
;  TITLE OF INVENTION:  ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
;  TITLE OF INVENTION:  USES
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE:  28341/6280JL
;  CURRENT APPLICATION NUMBER: US/09/794,748
;  CURRENT FILING DATE:  2001-02-27
;  PRIOR APPLICATION NUMBER:  09/416,901
;  PRIOR FILING DATE:  1999-10-13
;  PRIOR APPLICATION NUMBER:  60/155,493
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  09/404,133
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  PCT/US99/20881
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  60/101,594
;  PRIOR FILING DATE:  1998-09-24
;  NUMBER OF SEQ ID NOS:  73
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 27
;   LENGTH: 1278
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-794-748-27

Alignment Scores:
Pred. No.:                2.82e-14        Length:         1278
Score:                    144.00          Matches:        28
Percent Similarity:       100.00%         Conservative:   0
Best Local Similarity:    100.00%         Mismatches:     0
Query Match:              100.00%         Indels:         0
DB:                       9               Gaps:           0

US-10-726-967A-52 (1-28) x US-09-794-748-27 (1-1278)

Qy          1 GlyTyrTyrValGluMetThrValGlySerProProGlnThrLeuAsnIleLeuValAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGAT 195

Qy         21 ThrGlySerSerAsnPheAlaVal 28
              ||||||||||||||||||||||||||
Db        196 ACAGGCAGCAGTAACTTTGCAGTG 219

RESULT 5
US-09-794-925-27
; Sequence 27, Application US/09794925
; Patent No. US20020064819A1
; GENERAL INFORMATION:
;  APPLICANT:  Gurney, Mark E.
;  APPLICANT:  Bienkowski, Michael J.
;  APPLICANT:  Heinrikson, Robert L.
;  APPLICANT:  Parodi, Luis A.
;  APPLICANT:  Yan, Riqiang
;  TITLE OF INVENTION:  ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE:  28341/6280HI
;  CURRENT APPLICATION NUMBER: US/09/794,925
;  CURRENT FILING DATE:  2001-02-27
;  PRIOR APPLICATION NUMBER:  09/416,901
;  PRIOR FILING DATE:  1999-10-13
;  PRIOR APPLICATION NUMBER:  60/155,493
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  09/404,133
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  PCT/US99/20881
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  60/101,594
;  PRIOR FILING DATE:  1998-09-24
;  NUMBER OF SEQ ID NOS:  73
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 27
;   LENGTH: 1278
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-794-925-27

Alignment Scores:
Pred. No.:                2.82e-14        Length:         1278
Score:                    144.00          Matches:        28
Percent Similarity:       100.00%         Conservative:   0
Best Local Similarity:    100.00%         Mismatches:     0
Query Match:              100.00%         Indels:         0
DB:                       9               Gaps:           0

US-10-726-967A-52 (1-28) x US-09-794-925-27 (1-1278)

Qy          1 GlyTyrTyrValGluMetThrValGlySerProProGlnThrLeuAsnIleLeuValAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGAT 195

Qy         21 ThrGlySerSerAsnPheAlaVal 28
              ||||||||||||||||||||||||||
Db        196 ACAGGCAGCAGTAACTTTGCAGTG 219

RESULT 6
US-09-681-442-27
; Sequence 27, Application US/09681442
; Patent No. US20020081634A1
; GENERAL INFORMATION:
;  APPLICANT: Gurney, Mark E.
;  APPLICANT:  Bienkowski, Michael J.
;  APPLICANT:  Heinrikson, Robert L.
;  APPLICANT:  Parodi, Luis A.
;  APPLICANT:  Yan, Riqiang
;  TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE: 28341/6280FG
;  CURRENT APPLICATION NUMBER: US/09/681,442
;  CURRENT FILING DATE:  2001-04-05
;  PRIOR APPLICATION NUMBER: 09/416,901
;  PRIOR FILING DATE: 1999-10-13
;  PRIOR APPLICATION NUMBER: 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
;   LENGTH: 1278
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-681-442-27

Alignment Scores:
Pred. No.:                2.82e-14        Length:         1278
Score:                    144.00          Matches:        28
Percent Similarity:       100.00%         Conservative:   0
Best Local Similarity:    100.00%         Mismatches:     0
Query Match:              100.00%         Indels:         0
DB:                       9               Gaps:           0

US-10-726-967A-52 (1-28) x US-09-681-442-27 (1-1278)

Qy          1 GlyTyrTyrValGluMetThrValGlySerProProGlnThrLeuAsnIleLeuValAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGAT 195

Qy         21 ThrGlySerSerAsnPheAlaVal 28
              ||||||||||||||||||||||||||
```

```
Db        196 ACAGGCAGCAGTAACTTTGCAGTG 219

RESULT 7
US-09-869-414-27
; Sequence 27, Application US/09869414
; Publication No. US20030077226A1
; GENERAL INFORMATION:
;  APPLICANT: Beinkowski et al.
;  TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE: 28341/6280M
;  CURRENT APPLICATION NUMBER: US/09/869,414
;  CURRENT FILING DATE:  2001-06-27
;  PRIOR APPLICATION NUMBER: 09/416,901
;  PRIOR FILING DATE: 1999-10-13
;  PRIOR APPLICATION NUMBER: 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
;   LENGTH: 1278
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-869-414-27

Alignment Scores:
Pred. No.:                2.82e-14      Length:          1278
Score:                    144.00        Matches:         28
Percent Similarity:       100.00%       Conservative:    0
Best Local Similarity:    100.00%       Mismatches:      0
Query Match:              100.00%       Indels:          0
DB:                       10            Gaps:            0

US-10-726-967A-52 (1-28) x US-09-869-414-27 (1-1278)

Qy          1 GlyTyrTyrValGluMetThrValGlySerProProGlnThrLeuAsnIleLeuValAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGAT 195

Qy         21 ThrGlySerSerAsnPheAlaVal 28
              ||||||||||||||||||||||||||
Db        196 ACAGGCAGCAGTAACTTTGCAGTG 219

RESULT 8
US-09-548-366-27
; Sequence 27, Application US/09548366
; Publication No. US20030104365A1
; GENERAL INFORMATION:
;  APPLICANT:  Gurney, Mark E.
;  APPLICANT:  Bienkowski, Michael J.
;  APPLICANT:  Heinrikson, Robert L.
;  APPLICANT:  Parodi, Luis A.
;  APPLICANT:  Yan, Riqiang
;  TITLE OF INVENTION:  ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
;  TITLE OF INVENTION:  USES THEREFOR
;  FILE REFERENCE:  28341/6280A
;  CURRENT APPLICATION NUMBER: US/09/548,366
;  CURRENT FILING DATE:  2000-04-12
;  PRIOR APPLICATION NUMBER:  60/155,493
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  09/404,133
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  PCT/US99/20881
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  60/101,594
;  PRIOR FILING DATE:  1998-09-24
;  NUMBER OF SEQ ID NOS:  65
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 27
;   LENGTH: 1278
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-548-366-27

Alignment Scores:
Pred. No.:                2.82e-14      Length:          1278
Score:                    144.00        Matches:         28
Percent Similarity:       100.00%       Conservative:    0
Best Local Similarity:    100.00%       Mismatches:      0
Query Match:              100.00%       Indels:          0
DB:                       10            Gaps:            0

US-10-726-967A-52 (1-28) x US-09-548-366-27 (1-1278)

Qy          1 GlyTyrTyrValGluMetThrValGlySerProProGlnThrLeuAsnIleLeuValAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGAT 195

Qy         21 ThrGlySerSerAsnPheAlaVal 28
              ||||||||||||||||||||||||||
Db        196 ACAGGCAGCAGTAACTTTGCAGTG 219

RESULT 9
US-10-652-927-27
; Sequence 27, Application US/10652927
; Publication No. US20040043408A1
; GENERAL INFORMATION:
;  APPLICANT: Gurney et al.
;  TITLE OF INVENTION: Alzheimer's Disease Secretase, APP Substrates Therefor and Uses
;  TITLE OF INVENTION:  Therefor
;  FILE REFERENCE: 29915/6280N3
;  CURRENT APPLICATION NUMBER: US/10/652,927
;  CURRENT FILING DATE:  2003-08-29
;  PRIOR APPLICATION NUMBER: 09/794,925
;  PRIOR FILING DATE: 2001-02-27
;  PRIOR APPLICATION NUMBER: 09/416,901
;  PRIOR FILING DATE: 1999-10-13
;  PRIOR APPLICATION NUMBER: 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 74
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
;   LENGTH: 1278
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-652-927-27

Alignment Scores:
Pred. No.:                2.82e-14      Length:          1278
Score:                    144.00        Matches:         28
Percent Similarity:       100.00%       Conservative:    0
Best Local Similarity:    100.00%       Mismatches:      0
Query Match:              100.00%       Indels:          0
DB:                       18            Gaps:            0

US-10-726-967A-52 (1-28) x US-10-652-927-27 (1-1278)

Qy          1 GlyTyrTyrValGluMetThrValGlySerProProGlnThrLeuAsnIleLeuValAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGAT 195

Qy         21 ThrGlySerSerAsnPheAlaVal 28
              ||||||||||||||||||||||||||
Db        196 ACAGGCAGCAGTAACTTTGCAGTG 219
```

```
RESULT 10
US-10-652-830-27
; Sequence 27, Application US/10652830
; Publication No. US20040048303A1
; GENERAL INFORMATION:
;  APPLICANT: Gurney et al.
;  TITLE OF INVENTION: Alzheimer's Disease Secretase, APP Substrates Therefor and Uses
;  TITLE OF INVENTION:  Therefor
;  FILE REFERENCE: 29915/6280N1
;  CURRENT APPLICATION NUMBER: US/10/652,830
;  CURRENT FILING DATE:  2003-08-29
;  PRIOR APPLICATION NUMBER: 09/794,925
;  PRIOR FILING DATE: 2001-02-27
;  PRIOR APPLICATION NUMBER: 09/416,901
;  PRIOR FILING DATE: 1999-10-13
;  PRIOR APPLICATION NUMBER: 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 74
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
;   LENGTH: 1278
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-652-830-27

Alignment Scores:
Pred. No.:              2.82e-14      Length:          1278
Score:                  144.00        Matches:         28
Percent Similarity:     100.00%       Conservative:    0
Best Local Similarity:  100.00%       Mismatches:      0
Query Match:            100.00%       Indels:          0
DB:                     18            Gaps:            0

US-10-726-967A-52 (1-28) x US-10-652-830-27 (1-1278)

Qy          1 GlyTyrTyrValGluMetThrValGlySerProProGlnThrLeuAsnIleLeuValAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGAT 195

Qy         21 ThrGlySerSerAsnPheAlaVal 28
              ||||||||||||||||||||||||||
Db        196 ACAGGCAGCAGTAACTTTGCAGTG 219

RESULT 11
US-10-652-045-27
; Sequence 27, Application US/10652045
; Publication No. US20040166507A1
; GENERAL INFORMATION:
;  APPLICANT: Gurney et al.
;  TITLE OF INVENTION: Alzheimer's Disease Secretase, APP Substrates Therefor and Uses
;  TITLE OF INVENTION:  Therefor
;  FILE REFERENCE: 29915/6280N2
;  CURRENT APPLICATION NUMBER: US/10/652,045
;  CURRENT FILING DATE:  2003-08-29
;  PRIOR APPLICATION NUMBER: 09/794,925
;  PRIOR FILING DATE: 2001-02-27
;  PRIOR APPLICATION NUMBER: 09/416,901
;  PRIOR FILING DATE: 1999-10-13
;  PRIOR APPLICATION NUMBER: 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 74
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
;   LENGTH: 1278
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-652-045-27

Alignment Scores:
Pred. No.:              2.82e-14      Length:          1278
Score:                  144.00        Matches:         28
Percent Similarity:     100.00%       Conservative:    0
Best Local Similarity:  100.00%       Mismatches:      0
Query Match:            100.00%       Indels:          0
DB:                     19            Gaps:            0

US-10-726-967A-52 (1-28) x US-10-652-045-27 (1-1278)

Qy          1 GlyTyrTyrValGluMetThrValGlySerProProGlnThrLeuAsnIleLeuValAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGAT 195

Qy         21 ThrGlySerSerAsnPheAlaVal 28
              ||||||||||||||||||||||||||
Db        196 ACAGGCAGCAGTAACTTTGCAGTG 219

RESULT 12
US-10-476-935-27
; Sequence 27, Application US/10476935
; Publication No. US20040234976A1
; GENERAL INFORMATION:
;  APPLICANT: Beinkowski et al.
;  TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE: 28341/6280M1
;  CURRENT APPLICATION NUMBER: US/10/476,935
;  CURRENT FILING DATE:  2003-11-06
;  PRIOR APPLICATION NUMBER: 09/416,901
;  PRIOR FILING DATE: 1999-10-13
;  PRIOR APPLICATION NUMBER: 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
;   LENGTH: 1278
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-476-935-27

Alignment Scores:
Pred. No.:              2.82e-14      Length:          1278
Score:                  144.00        Matches:         28
Percent Similarity:     100.00%       Conservative:    0
Best Local Similarity:  100.00%       Mismatches:      0
Query Match:            100.00%       Indels:          0
DB:                     20            Gaps:            0

US-10-726-967A-52 (1-28) x US-10-476-935-27 (1-1278)

Qy          1 GlyTyrTyrValGluMetThrValGlySerProProGlnThrLeuAsnIleLeuValAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGAT 195

Qy         21 ThrGlySerSerAsnPheAlaVal 28
              ||||||||||||||||||||||||||
Db        196 ACAGGCAGCAGTAACTTTGCAGTG 219
```

RESULT 13
US-10-940-867-27
; Sequence 27, Application US/10940867
; Publication No. US20050026256A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; APPLICANT: Pharmacia & Upjohn Company
; TITLE OF INVENTION: Alzheimer's Disease Secretase
; FILE REFERENCE: 6177.PCPA
; CURRENT APPLICATION NUMBER: US/10/940,867
; CURRENT FILING DATE: 2004-09-14
; PRIOR APPLICATION NUMBER: US 09/806,194
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 1278
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-940-867-27

Alignment Scores:

Pred. No.:	2.82e-14	Length:	1278
Score:	144.00	Matches:	28
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	21	Gaps:	0

US-10-726-967A-52 (1-28) x US-10-940-867-27 (1-1278)

```
Qy          1 GlyTyrTyrValGluMetThrValGlySerProProGlnThrLeuAsnIleLeuValAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCCCGCAGACGCTCAACATCCTGGTGGAT 195

Qy         21 ThrGlySerSerAsnPheAlaVal 28
              |||||||||||||||||||||||||
Db        196 ACAGGCAGCAGTAACTTTGCAGTG 219
```

RESULT 14
US-10-477-076-27
; Sequence 27, Application US/10477076
; Publication No. US20050080232A1
; GENERAL INFORMATION:
; APPLICANT: Beinkowski et al.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280M2
; CURRENT APPLICATION NUMBER: US/10/477,076
; CURRENT FILING DATE: 2003-11-06
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 1278
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-477-076-27

Alignment Scores:

Pred. No.:	2.82e-14	Length:	1278
Score:	144.00	Matches:	28
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	21	Gaps:	0

US-10-726-967A-52 (1-28) x US-10-477-076-27 (1-1278)

```
Qy          1 GlyTyrTyrValGluMetThrValGlySerProProGlnThrLeuAsnIleLeuValAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCCCGCAGACGCTCAACATCCTGGTGGAT 195

Qy         21 ThrGlySerSerAsnPheAlaVal 28
              |||||||||||||||||||||||||
Db        196 ACAGGCAGCAGTAACTTTGCAGTG 219
```

RESULT 15
US-09-794-927-50
; Sequence 50, Application US/09794927
; Patent No. US20010016324A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280FG
; CURRENT APPLICATION NUMBER: US/09/794,927
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 50
; LENGTH: 1287
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Hu-Asp2(b)
; OTHER INFORMATION: delta TM
US-09-794-927-50

Alignment Scores:

Pred. No.:	2.84e-14	Length:	1287
Score:	144.00	Matches:	28
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-10-726-967A-52 (1-28) x US-09-794-927-50 (1-1287)

```
Qy          1 GlyTyrTyrValGluMetThrValGlySerProProGlnThrLeuAsnIleLeuValAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        220 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCCCGCAGACGCTCAACATCCTGGTGGAT 279

Qy         21 ThrGlySerSerAsnPheAlaVal 28
              |||||||||||||||||||||||||
Db        280 ACAGGCAGCAGTAACTTTGCAGTG 303
```

Search completed: July 27, 2005, 19:03:20
Job time : 629 secs

GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: July 27, 2005, 13:56:30 ; Search time 3149 Seconds
(without alignments)
338.457 Million cell updates/sec

Title: US-10-726-967A-52
Perfect score: 144
Sequence: 1 GYYVEMTVGSPPQTLNILVDTGSSNFAV 28

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US10726967/runat_26072005_130734_6151/app_query.fasta_1.199
-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10726967_@CGN_1_1_5180_@runat_26072005_130734_6151 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	144	100.0	346	5	BY103030	BY103030 BY103030
2	144	100.0	365	5	BY080676	BY080676 BY080676
3	144	100.0	1123	5	BX376891	BX376891 BX376891
4	144	100.0	1506	9	AY417360	AY417360 Homo sapi
5	144	100.0	1506	9	AY417362	AY417362 Mus muscu
6	144	100.0	3634	3	AK041285	AK041285 Mus muscu
7	144	100.0	3805	3	AK082230	AK082230 Mus muscu
8	144	100.0	3859	3	AK014464	AK014464 Mus muscu
9	144	100.0	3877	3	AK033112	AK033112 Mus muscu
10	144	100.0	3880	3	AK080498	AK080498 Mus muscu
11	144	100.0	4048	3	AK082317	AK082317 Mus muscu
12	144	100.0	4101	3	AK046175	AK046175 Mus muscu
13	143	99.3	4046	3	AK049626	AK049626 Mus muscu
14	138	95.8	461	1	AL700831	AL700831 DKFZp686I
15	138	95.8	720	4	BG288435	BG288435 602383404
16	138	95.8	813	7	CN224123	CN224123 WLA053E12
17	137	95.1	458	1	AL700814	AL700814 DKFZp686H
18	130	90.3	611	7	CN484125	CN484125 hw42d08.y
19	128	88.9	727	6	CA749486	CA749486 UI-M-FY0-
20	125	86.8	1001	5	BU128383	BU128383 603113984
21	124	86.1	761	7	CN064831	CN064831 Ag2_p8_P2
22	124	86.1	763	7	CN064511	CN064511 Ag2_p7_F9
23	124	86.1	817	7	CK139305	CK139305 AGENCOURT
24	124	86.1	819	7	CK143759	CK143759 AGENCOURT
25	124	86.1	873	6	CD755522	CD755522 AGENCOURT
26	124	86.1	893	6	CA475986	CA475986 AGENCOURT
27	124	86.1	898	6	CD757678	CD757678 AGENCOURT
28	124	86.1	915	6	CD756050	CD756050 AGENCOURT
29	122	84.7	880	5	BQ733989	BQ733989 AGENCOURT
30	120	83.3	556	1	AL788837	AL788837 AL788837
31	120	83.3	670	6	CA375995	CA375995 654231 NC
32	119	82.6	208	1	AI290317	AI290317 qm02b05.x
33	119	82.6	542	2	BE668968	BE668968 159420 MA
34	119	82.6	614	2	AW153854	AW153854 fi26d02.y
35	119	82.6	648	5	BM957312	BM957312 fy76f05.y
36	119	82.6	705	5	BP434294	BP434294 BP434294
37	119	82.6	712	7	CK681409	CK681409 ZF101-P00
38	119	82.6	751	7	CV480976	CV480976 AGENCOURT
39	119	82.6	765	4	BM006442	BM006442 603615166
40	119	82.6	778	7	CN016970	CN016970 AGENCOURT
41	119	82.6	783	6	CB962018	CB962018 AGENCOURT
42	119	82.6	795	6	CB998213	CB998213 AGENCOURT
43	119	82.6	814	6	CB996886	CB996886 AGENCOURT
44	119	82.6	847	7	CK871931	CK871931 AGENCOURT
45	119	82.6	847	7	CN021417	CN021417 AGENCOURT

ALIGNMENTS

RESULT 1
BY103030
LOCUS BY103030 346 bp mRNA linear EST 07-DEC-2002
DEFINITION BY103030 RIKEN full-length enriched, pooled tissues, adult spleen, etc. Mus musculus cDNA clone K630148P20 5', mRNA sequence.
ACCESSION BY103030
VERSION BY103030.1 GI:26213647
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 346)
AUTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I.,

Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

MEDLINE 22354683

PUBMED 12466851

COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

FEATURES Location/Qualifiers

source 1. .346
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="K630148P20"
/clone_lib="RIKEN full-length enriched, pooled tissues, adult spleen, etc."
/note="(dev_stage=adult,tissue_type=spleen,sex=male), (dev_stage=adult,tissue_type=kidney,sex=male), (dev_stage=adult,tissue_type=testis,sex=male), (dev_stage=adult,tissue_type=thymus,sex=male), (dev_stage=adult,tissue_type=heart,sex=male), (dev_stage=adult,tissue_type=colon,sex=male), (dev_stage=adult,tissue_type=stomach,sex=male), (dev_stage=adult,tissue_type=liver,sex=male), (dev_stage=13 days embryo,tissue_type=whole body,sex=mix),(dev_stage=14 days embryo,tissue_type=whole body,sex=mix),(dev_stage=16 days embryo,tissue_type=whole body,sex=mix),(dev_stage=17 days embryo,tissue_type=whole body,sex=mix),(dev_stage=15 days pregnant, adult,tissue_type=amnion,sex=female),(dev_stage=10 days neonate,tissue_type=brain,sex=mix),(dev_stage=10 days neonate,tissue_type=thymus,sex=mix),(dev_stage=10 days neonate,tissue_type=heart,sex=mix)"

ORIGIN

Alignment Scores:
Pred. No.: 1.7e-13 Length: 346

Score: 144.00 Matches: 28
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 5 Gaps: 0

US-10-726-967A-52 (1-28) x BY103030 (1-346)

```
Qy          1 GlyTyrTyrValGluMetThrValGlySerProProGlnThrLeuAsnIleLeuValAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         86 GGCTACTATGTGGAGATGACCGTAGGCAGCCCCCCACAGACGCTCAACATCCTGGTGGAC 145

Qy         21 ThrGlySerSerAsnPheAlaVal 28
              ||||||||||||||||||||||||
Db        146 ACGGGCAGTAGTAACTTTGCAGTG 169
```

RESULT 2
BY080676
LOCUS BY080676 365 bp mRNA linear EST 07-DEC-2002
DEFINITION BY080676 RIKEN full-length enriched, 16 days embryo whole body Mus musculus cDNA clone K630026J04 5', mRNA sequence.
ACCESSION BY080676
VERSION BY080676.1 GI:26191219
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 365)
AUTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
MEDLINE 22354683
PUBMED 12466851
COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,

Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

FEATURES Location/Qualifiers
source 1. .365
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="K630026J04"
/tissue_type="whole body"
/dev_stage="16 days embryo"
/clone_lib="RIKEN full-length enriched, 16 days embryo whole body"

ORIGIN

Alignment Scores:

Pred. No.:	1.81e-13	Length:	365
Score:	144.00	Matches:	28
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	5	Gaps:	0

US-10-726-967A-52 (1-28) x BY080676 (1-365)

```
Qy          1 GlyTyrTyrValGluMetThrValGlySerProProGlnThrLeuAsnIleLeuValAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         86 GGCTACTATGTGGAGATGACCGTAGGCAGCCCCCCACAGACGCTCAACATCCTGGTGGAC 145

Qy         21 ThrGlySerSerAsnPheAlaVal 28
              |||||||||||||||||||||||||
Db        146 ACGGGCAGTAGTAACTTTGCAGTG 169
```

RESULT 3
BX376891
LOCUS BX376891 1123 bp mRNA linear EST 23-APR-2004
DEFINITION BX376891 Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED Homo sapiens cDNA clone CS0DD007YP18 5-PRIME, mRNA sequence.
ACCESSION BX376891
VERSION BX376891.2 GI:46556538
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1123)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On May 8, 2003 this sequence version replaced gi:30434929.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 5902.r
For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CS0DD007DH09QP1&c=5902.r.

FEATURES Location/Qualifiers
source 1. .1123
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DD007YP18"
/tissue_type="NEUROBLASTOMA COT 50-NORMALIZED"
/clone_lib="Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Alignment Scores:

Pred. No.:	7.08e-13	Length:	1123
Score:	144.00	Matches:	28
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	5	Gaps:	0

US-10-726-967A-52 (1-28) x BX376891 (1-1123)

```
Qy          1 GlyTyrTyrValGluMetThrValGlySerProProGlnThrLeuAsnIleLeuValAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        657 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGAT 716

Qy         21 ThrGlySerSerAsnPheAlaVal 28
              |||||||||||||||||||||||||
Db        717 ACAGGCAGCAGTAACTTTGCAGTG 740
```

RESULT 4
AY417360
LOCUS AY417360 1506 bp DNA linear GSS 17-DEC-2003
DEFINITION Homo sapiens BACE gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
ACCESSION AY417360
VERSION AY417360.1 GI:39773320
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1506)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1506)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES Location/Qualifiers
source 1. .1506
/organism="Homo sapiens"

/mol_type="genomic DNA"
/db_xref="taxon:9606"
gene <1..>1506
/gene="BACE"
/locus_tag="HCM6198"
ORIGIN

Alignment Scores:
Pred. No.: 1.01e-12 Length: 1506
Score: 144.00 Matches: 28
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-726-967A-52 (1-28) x AY417360 (1-1506)

Qy 1 GlyTyrTyrValGluMetThrValGlySerProProGlnThrLeuAsnIleLeuValAsp 20
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 220 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGAT 279

Qy 21 ThrGlySerSerAsnPheAlaVal 28
|||||||||||||||||||||||||||
Db 280 ACAGGCAGCAGTAACTTTGCAGTG 303

RESULT 5
AY417362
LOCUS AY417362 1506 bp DNA linear GSS 17-DEC-2003
DEFINITION Mus musculus BACE gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
ACCESSION AY417362
VERSION AY417362.1 GI:39773322
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1506)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1506)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.
FEATURES Location/Qualifiers
source 1..1506
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
gene <1..>1506
/gene="BACE"
/locus_tag="HCM6198"
ORIGIN

Alignment Scores:
Pred. No.: 1.01e-12 Length: 1506
Score: 144.00 Matches: 28
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-726-967A-52 (1-28) x AY417362 (1-1506)

Qy 1 GlyTyrTyrValGluMetThrValGlySerProProGlnThrLeuAsnIleLeuValAsp 20
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 220 GGCTACTATGTGGAGATGACCGTAGGCAGCCCCCCACAGACGCTCAACATCCTGGTGGAC 279

Qy 21 ThrGlySerSerAsnPheAlaVal 28
|||||||||||||||||||||||||||
Db 280 ACGGGCAGTAGTAACTTTGCAGTG 303

RESULT 6
AK041285
LOCUS AK041285 3634 bp mRNA linear HTC 03-APR-2004
DEFINITION Mus musculus adult male aorta and vein cDNA, RIKEN full-length enriched library, clone:A530097B07 product:beta-site APP cleaving enzyme, full insert sequence.
ACCESSION AK041285
VERSION AK041285.1 GI:26334342
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
REFERENCE 4
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
REFERENCE 5
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
REFERENCE 6 (bases 1 to 3634)
AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,

```
            Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
            Muramatsu,M. and Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
            URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.jp/
            URL:http://fantom.gsc.riken.jp/.
FEATURES             Location/Qualifiers
     source          1. .3634
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="FANTOM_DB:A530097B07"
                     /db_xref="taxon:10090"
                     /clone="A530097B07"
                     /sex="male"
                     /tissue_type="aorta and vein"
                     /clone_lib="RIKEN full-length enriched mouse cDNA library"
                     /dev_stage="adult"
     CDS             450. .1955
                     /note="unnamed protein product; beta-site APP cleaving
                     enzyme (MGD|MGI:1346542, GB|NM_011792, evidence: BLASTN,
                     98%, match=3874)
                     putative"
                     /codon_start=1
                     /protein_id="BAC30889.1"
                     /db_xref="GI:26334343"
                     /translation="MAPALHWLLLWVGSGMLPAQGTHLGIRLPLRSGLAGPPLGLRLP
                     RETDEESEEPGRRGSFVEMVDNLRGKSGQGYYVEMTVGSPPQTLNILVDTGSSNFAVG
                     AAPHPFLHRYYQRQLSSTYRDLRKGVYVPYTQGKWEGELGTDLVSIPHGPNVTVRANI
                     AAITESDKFFINGSNWEGILGLAYAEIARPDDSLEPFFDSLVKQTHIPNIFSLQLCGA
                     GFPLNQTEALASVGGSMIIGGIDHSLYTGSLWYTPIRREWYYEVIIVRVEINGQDLKM
                     DCKEYNYDKSIVDSGTTNLRLPKKVFEAAVKSIKAASSTEKFPDGFWLGEQLVCWQAG
                     TTPWNIFPVISLYLMGEVTNQSFRITILPQQYLRPVEDVATSQDDCYKFAVSQSSTGT
                     VMGAVIMEGFYVVFDRARKRIGFAVSACHVHDEFRTAAVEGPFVTADMEDCGYNIPQT
                     DESTLMTIAYVMAAICALFMLPLCLMVCQWRCLRCLRHQHDDFADDISLLK"
ORIGIN

Alignment Scores:
Pred. No.:                2.94e-12        Length:          3634
Score:                    144.00          Matches:         28
Percent Similarity:       100.00%         Conservative:    0
Best Local Similarity:    100.00%         Mismatches:      0
Query Match:              100.00%         Indels:          0
DB:                       3               Gaps:            0

US-10-726-967A-52 (1-28) x AK041285 (1-3634)

Qy          1 GlyTyrTyrValGluMetThrValGlySerProProGlnThrLeuAsnIleLeuValAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        669 GGCTACTATGTGGAGATGACCGTAGGCAGCCCCCCACAGACGCTCAACATCCTGGTGGAC 728

Qy         21 ThrGlySerSerAsnPheAlaVal 28
              |||||||||||||||||||||||||
Db        729 ACGGGCAGTAGTAACTTTGCAGTG 752

RESULT 7
AK082230
LOCUS       AK082230               3805 bp    mRNA    linear   HTC 03-APR-2004
DEFINITION  Mus musculus 0 day neonate cerebellum cDNA, RIKEN full-length
            enriched library, clone:C230026O08 product:beta-site APP cleaving
            enzyme, full insert sequence.
ACCESSION   AK082230
VERSION     AK082230.1  GI:26100512
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   20530913
   PUBMED   11076861
REFERENCE   4
  AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5
  AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6  (bases 1 to 3805)
  AUTHORS   Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
            Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
            Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
            Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
            Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
            Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
            Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
            Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
            Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
            Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
            Muramatsu,M. and Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
            URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.jp/
```

URL:http://fantom.gsc.riken.jp/.

FEATURES Location/Qualifiers
source 1. .3805
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="FANTOM_DB:C230026O08"
/db_xref="taxon:10090"
/clone="C230026O08"
/tissue_type="cerebellum"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="0 day neonate"
misc_feature 448. .1955
/note="beta-site APP cleaving enzyme (MGD|MGI:1346542, GB|NM_011792, evidence: BLASTN, 98%, match=3874) putative"
ORIGIN

Alignment Scores:

Pred. No.:	3.11e-12	Length:	3805
Score:	144.00	Matches:	28
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	3	Gaps:	0

US-10-726-967A-52 (1-28) x AK082230 (1-3805)

```
Qy          1 GlyTyrTyrValGluMetThrValGlySerProProGlnThrLeuAsnIleLeuValAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 GGCTACTATGTGGAGATGACCGTAGGCAGCCCCCCACAGACGCTCAACATCCTGGTGGAC 726

Qy         21 ThrGlySerSerAsnPheAlaVal 28
              |||||||||||||||||||||||||
Db        727 ACGGGCAGTAGTAACTTTGCAGTG 750
```

RESULT 8
AK014464
LOCUS AK014464 3859 bp mRNA linear HTC 03-APR-2004
DEFINITION Mus musculus 16 days embryo head cDNA, RIKEN full-length enriched library, clone:4122401C04 product:beta-site APP cleaving enzyme, full insert sequence.
ACCESSION AK014464
VERSION AK014464.1 GI:12852334
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
REFERENCE 4
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
REFERENCE 5
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
REFERENCE 6 (bases 1 to 3859)
AUTHORS Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Arai,A., Aono,H., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
TITLE Direct Submission
JOURNAL Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
COMMENT Please visit our web site (http://genome.gsc.riken.jp/) for further details.
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCC 3']. cDNA was cleaved with BamHI and XhoI. cDNA of size comprised longer than 7 kb was selected before cloning. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI. Host: DH10B.
FEATURES Location/Qualifiers
source 1. .3859
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="FANTOM_DB:4122401C04"
/db_xref="taxon:10090"
/clone="4122401C04"
/tissue_type="head"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="16 days embryo"
CDS 430. .1935
/note="unnamed protein product; beta-site APP cleaving enzyme (MGD|MGI:1346542, GB|NM_011792, evidence: BLASTN, 98%, match=3874) putative"
/codon_start=1
/protein_id="BAB29370.1"
/db_xref="GI:12852335"
/translation="MAPALHWLLLWVGSGMLPAQGTHLGIRLPLRSGLAGPPLGLRLP
RETDEESEEPGRRGSFVEMVDNLRGKSGQGYYVEMTVGSPPQTLNILVDTGSSNFAVG
AAPHPFLHRYYQRQLSSTYRDLRKGVYVPYTQGKWEGELGTDLVSIPHGPNVTVRANI

AAITESDKFFINGSNWEGILGLAYAEIARPDDSLEPFFDSLVKQTHIPNIFSLQLCGA
GFPLNQTEALASVGGSMIIGGIDHSLYTGSLWYTPIRREWYYEVIIVRVEINGQDLKM
DCKEYNYDKSIVDSGTTNLRLPKKVFEAAVKSIKAASSTEKFPDGFWLGEQLVCWQAG
TTPWNIFPVISLYLMGEVTNQSFRITILPQQYLRPVEDVATSQDDCYKFAVSQSSTGT
VMGAVIMEGFYVVFDRARKRIGFAVSACHVHDEFRTAAVEGPFVTADMEDCGYNIPQT
DESTLMTIAYVMAAICALFMLPLCLMVCQWRCLRCLRHQHDDFADDISLLK"

ORIGIN

Alignment Scores:

Pred. No.:	3.16e-12	Length:	3859
Score:	144.00	Matches:	28
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	3	Gaps:	0

US-10-726-967A-52 (1-28) x AK014464 (1-3859)

```
Qy          1 GlyTyrTyrValGluMetThrValGlySerProProGlnThrLeuAsnIleLeuValAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        649 GGCTACTATGTGGAGATGACCGTAGGCAGCCCCCCACAGACGCTCAACATCCTGGTGGAC 708

Qy         21 ThrGlySerSerAsnPheAlaVal 28
              |||||||||||||||||||||||||
Db        709 ACGGGCAGTAGTAACTTTGCAGTG 732
```

RESULT 9
AK033112
LOCUS AK033112 3877 bp mRNA linear HTC 03-APR-2004
DEFINITION Mus musculus 15 days embryo male testis cDNA, RIKEN full-length enriched library, clone:8030431G04 product:beta-site APP cleaving enzyme, full insert sequence.
ACCESSION AK033112
VERSION AK033112.1 GI:26328834
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
REFERENCE 4
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
REFERENCE 5
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
REFERENCE 6 (bases 1 to 3877)
AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
TITLE Direct Submission
JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
FEATURES Location/Qualifiers
source 1. .3877
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="FANTOM_DB:8030431G04"
/db_xref="taxon:10090"
/clone="8030431G04"
/sex="male"
/tissue_type="testis"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="15 days embryo"
CDS 450. .1955
/note="unnamed protein product; beta-site APP cleaving enzyme (MGD|MGI:1346542, GB|NM_011792, evidence: BLASTN, 98%, match=3874)
putative"
/codon_start=1
/protein_id="BAC28156.1"
/db_xref="GI:26328835"
/translation="MAPALHWLLLWVGSGMLPAQGTHLGIRLPLRSGLAGPPLGLRLP
RETDEESEEPGRRGSFVEMVDNLRGKSGQGYYVEMTVGSPPQTLNILVDTGSSNFAVG
AAPHPFLHRYYQRQLSSTYRDLRKGVYVPYTQGKWEGELGTDLVSIPHGPNVTVRANI
AAITESDKFFINGSNWEGILGLAYAEIARPDDSLEPFFDSLVKQTHIPNIFSLQLCGA
GFPLNQTEALASVGGSMIIGGIDHSLYTGSLWYTPIRREWYYEVIIVRVEINGQDLKM
DCKEYNYDKSIVDSGTTNLRLPKKVFEAAVKSIKAASSTEKFPDGFWLGEQLVCWQAG
TTPWNIFPVISLYLMGEVTNQSFRITILPQQYLRPVEDVATSQDDCYKFAVSQSSTGT
VMGAVIMEGFYVVFDRARKRIGFAVSACHVHDEFRTAAVEGPFVTADMEDCGYNIPQT
DESTLMTIAYVMAAICALFMLPLCLMVCQWRCLRCLRHQHDDFADDISLLK"

ORIGIN

Alignment Scores:

Pred. No.:	3.18e-12	Length:	3877
Score:	144.00	Matches:	28
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	3	Gaps:	0

US-10-726-967A-52 (1-28) x AK033112 (1-3877)

```
Qy          1 GlyTyrTyrValGluMetThrValGlySerProProGlnThrLeuAsnIleLeuValAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        669 GGCTACTATGTGGAGATGACCGTAGGCAGCCCCCCACAGACGCTCAACATCCTGGTGGAC 728

Qy         21 ThrGlySerSerAsnPheAlaVal 28
              |||||||||||||||||||||||||
Db        729 ACGGGCAGTAGTAACTTTGCAGTG 752

RESULT 10
AK080498
LOCUS       AK080498               3880 bp    mRNA    linear   HTC 03-APR-2004
DEFINITION  Mus musculus 7 days neonate cerebellum cDNA, RIKEN full-length
            enriched library, clone:A730059K08 product:beta-site APP cleaving
            enzyme, full insert sequence.
ACCESSION   AK080498
VERSION     AK080498.1  GI:26099278
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   20530913
   PUBMED   11076861
REFERENCE   4
  AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5
  AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6  (bases 1 to 3880)
  AUTHORS   Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
            Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
            Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
            Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
            Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
            Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
            Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
            Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
            Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
            Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
            Muramatsu,M. and Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
            URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.jp/
            URL:http://fantom.gsc.riken.jp/.
FEATURES                Location/Qualifiers
     source             1. .3880
                        /organism="Mus musculus"
                        /mol_type="mRNA"
                        /strain="C57BL/6J"
                        /db_xref="FANTOM_DB:A730059K08"
                        /db_xref="taxon:10090"
                        /clone="A730059K08"
                        /tissue_type="cerebellum"
                        /clone_lib="RIKEN full-length enriched mouse cDNA library"
                        /dev_stage="7 days neonate"
     misc_feature       450. .1957
                        /note="beta-site APP cleaving enzyme (MGD|MGI:1346542,
                        GB|NM_011792, evidence: BLASTN, 98%, match=3874)
                        putative"
ORIGIN

Alignment Scores:
Pred. No.:                3.18e-12        Length:          3880
Score:                    144.00          Matches:         28
Percent Similarity:       100.00%         Conservative:    0
Best Local Similarity:    100.00%         Mismatches:      0
Query Match:              100.00%         Indels:          0
DB:                       3               Gaps:            0

US-10-726-967A-52 (1-28) x AK080498 (1-3880)

Qy          1 GlyTyrTyrValGluMetThrValGlySerProProGlnThrLeuAsnIleLeuValAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        671 GGCTACTATGTGGAGATGACCGTAGGCAGCCCCCCACAGACGCTCAACATCCTGGTGGAC 730

Qy         21 ThrGlySerSerAsnPheAlaVal 28
              |||||||||||||||||||||||||
Db        731 ACGGGCAGTAGTAACTTTGCAGTG 754

RESULT 11
AK082317
LOCUS       AK082317               4048 bp    mRNA    linear   HTC 03-APR-2004
DEFINITION  Mus musculus 0 day neonate cerebellum cDNA, RIKEN full-length
            enriched library, clone:C230037E16 product:beta-site APP cleaving
            enzyme, full insert sequence.
ACCESSION   AK082317
VERSION     AK082317.1  GI:26349644
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
```

```
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   20530913
   PUBMED   11076861
REFERENCE   4
  AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5
  AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6  (bases 1 to 4048)
  AUTHORS   Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
            Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
            Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
            Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
            Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
            Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
            Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
            Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
            Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
            Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
            Muramatsu,M. and Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
            URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.jp/
            URL:http://fantom.gsc.riken.jp/.
FEATURES             Location/Qualifiers
     source          1. .4048
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="FANTOM_DB:C230037E16"
                     /db_xref="taxon:10090"
                     /clone="C230037E16"
                     /tissue_type="cerebellum"
                     /clone_lib="RIKEN full-length enriched mouse cDNA library"
                     /dev_stage="0 day neonate"
     CDS             451. .1854
                     /note="unnamed protein product; beta-site APP cleaving
                     enzyme (MGD|MGI:1346542, GB|NM_011792, evidence: BLASTN,
                     98%, match=3874)
                     putative"
                     /codon_start=1
                     /protein_id="BAC38462.1"
                     /db_xref="GI:26349645"
                     /translation="MAPALHWLLLWVGSGMLPAQGTHLGIRLPLRSGLAGPPLGLRLP
                     RETDEESEEPGRRGSFVEMVDNLRGKSGQGYYVEMTVGSPPQTLNILVDTGSSNFAVG
                     AAPHPFLHRYYQRQLSSTYRDLRKGVYVPYTQGKWEGELGTDLVSIPHGPNVTVRANI
                     AAITESDKFFINGSNWEGILGLAYAEIARPDDSLEPFFDSLVKQTHIPNIFSLQLCGA
                     GFPLNQTEALASVGGSMIIGGIDHSLYTGSLWYTPIRREWYYEVIIVRVEINGQDLKM
                     DCKETEKFPDGFWLGEQLVCWQAGTTPWNIFPVISLYLMGEVTNQSFRITILPQQYLR
                     PVEDVATSQDDCYKFAVSQSSTGTVMGAVIMEGFYVVFDRARKRIGFAVSACHVHDEF
                     RTAAVEGPFVTADMEDCGYNIPQTDESTLMTIAYVMAAICALFMLPLCLMVCQWRCLR
                     CLRHQHDDFADDISLLK"
ORIGIN

Alignment Scores:
Pred. No.:                3.35e-12        Length:          4048
Score:                    144.00          Matches:         28
Percent Similarity:       100.00%         Conservative:    0
Best Local Similarity:    100.00%         Mismatches:      0
Query Match:              100.00%         Indels:          0
DB:                       3               Gaps:            0

US-10-726-967A-52 (1-28) x AK082317 (1-4048)

Qy          1 GlyTyrTyrValGluMetThrValGlySerProProGlnThrLeuAsnIleLeuValAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        670 GGCTACTATGTGGAGATGACCGTAGGCAGCCCCCCACAGACGCTCAACATCCTGGTGGAC 729

Qy         21 ThrGlySerSerAsnPheAlaVal 28
              |||||||||||||||||||||||||
Db        730 ACGGGCAGTAGTAACTTTGCAGTG 753

RESULT 12
AK046175
LOCUS       AK046175                4101 bp    mRNA    linear   HTC 03-APR-2004
DEFINITION  Mus musculus adult male corpora quadrigemina cDNA, RIKEN
            full-length enriched library, clone:B230346M13 product:beta-site
            APP cleaving enzyme, full insert sequence.
ACCESSION   AK046175
VERSION     AK046175.1  GI:26337868
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   20530913
   PUBMED   11076861
```

```
REFERENCE   4
  AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5
  AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6  (bases 1 to 4101)
  AUTHORS   Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
            Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
            Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
            Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
            Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
            Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
            Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
            Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
            Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
            Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
            Muramatsu,M. and Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
            URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.jp/
            URL:http://fantom.gsc.riken.jp/.
FEATURES                Location/Qualifiers
     source             1. .4101
                        /organism="Mus musculus"
                        /mol_type="mRNA"
                        /strain="C57BL/6J"
                        /db_xref="FANTOM_DB:B230346M13"
                        /db_xref="taxon:10090"
                        /clone="B230346M13"
                        /sex="male"
                        /tissue_type="corpora quadrigemina"
                        /clone_lib="RIKEN full-length enriched mouse cDNA library"
                        /dev_stage="adult"
     CDS                447. .1952
                        /note="unnamed protein product; beta-site APP cleaving
                        enzyme (MGD|MGI:1346542, GB|NM_011792, evidence: BLASTN,
                        98%, match=3874)
                        putative"
                        /codon_start=1
                        /protein_id="BAC32620.1"
                        /db_xref="GI:26337869"
                        /translation="MAPALHWLLLWVGSGMLPAQGTHLGIRLPLRSGLAGPPLGLRLP
                        RETDEESEEPGRRGSFVEMVDNLRGKSGQGYYVEMTVGSPPQTLNILVDTGSSNFAVG
                        AAPHPFLHRYYQRQLSSTYRDLRKGVYVPYTQGKWEGELGTDLVSIPHGPNVTVRANI
                        AAITESDKFFINGSNWEGILGLAYAEIARPDDSLEPFFDSLVKQTHIPNIFSLQLCGA
                        GFPLNQTEALASVGGSMIIGGIDHSLYTGRLWYTPIRREWYYEVIIVRVEINGQDLKM
                        DCKEYNYDKSIVDSGTTNLRLPKKVFEAAVKSIKAASSTEKFPDGFWLGEQLVCWQAG
                        TTPWNIFPVISLYLMGEVTNQSFRITILPQQYLRPVEDVATSQDDCYKFAVSQSSTGT
                        VMGAVIMEGFYVVFDRARKRIGFAVSACHVHDEFRTAAVEGPFVTADMEDCGYNIPQT
                        DESTLMTIAYVMAAICALFMLPLCLMVCQWRCLRCLRHQHDDFADDISLLK"
ORIGIN

Alignment Scores:
Pred. No.:              3.4e-12         Length:         4101
```

```
Score:                  144.00          Matches:        28
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     3               Gaps:           0

US-10-726-967A-52 (1-28) x AK046175 (1-4101)

Qy          1 GlyTyrTyrValGluMetThrValGlySerProProGlnThrLeuAsnIleLeuValAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 GGCTACTATGTGGAGATGACCGTAGGCAGCCCCCCACAGACGCTCAACATCCTGGTGGAC 725

Qy         21 ThrGlySerSerAsnPheAlaVal 28
              |||||||||||||||||||||||||
Db        726 ACGGGCAGTAGTAACTTTGCAGTG 749

RESULT 13
AK049626
LOCUS       AK049626                4046 bp    mRNA    linear   HTC 03-APR-2004
DEFINITION  Mus musculus 12 days embryo spinal cord cDNA, RIKEN full-length
            enriched library, clone:C530008K17 product:beta-site APP cleaving
            enzyme, full insert sequence.
ACCESSION   AK049626
VERSION     AK049626.1  GI:26340361
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   20530913
   PUBMED   11076861
REFERENCE   4
  AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5
  AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6  (bases 1 to 4046)
  AUTHORS   Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
            Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
            Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
            Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
            Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
```

```
            Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
            Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
            Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
            Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
            Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
            Muramatsu,M. and Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
            URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.jp/
            URL:http://fantom.gsc.riken.jp/.
FEATURES             Location/Qualifiers
     source          1. .4046
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="FANTOM_DB:C530008K17"
                     /db_xref="taxon:10090"
                     /clone="C530008K17"
                     /tissue_type="spinal cord"
                     /clone_lib="RIKEN full-length enriched mouse cDNA library"
                     /dev_stage="12 days embryo"
     CDS             433. .1938
                     /note="unnamed protein product; beta-site APP cleaving
                     enzyme (MGD|MGI:1346542, GB|NM_011792, evidence: BLASTN,
                     98%, match=3874)
                     putative"
                     /codon_start=1
                     /protein_id="BAC33844.1"
                     /db_xref="GI:26340362"
                     /translation="MAPALHWLLLWVGSGMLPAQGTHLGIRLPLRSGLAGPPLGLRLP
                     RETDEESEEPGRRGSFVEMVDNLRGKSGQGYYVEMTIGSPPQTLNILVDTGSSNFAVG
                     AAPHPFLHRYYQRQLSSTYRDLRKGVYVPYTQGKWEGELGTDLVSIPHGPNVTVRANI
                     AAITESDKFFINGSNWEGILGLAYAEIARPDDSLEPFFDSLVKQTHIPNIFSLQLCGA
                     GFPLNQTEALASVGGSMIIGGIDHSLYTGSLWYTPIRREWYYEVIIVRVEINGQDLKM
                     DCKEYNYDKSIVDSGTTNLRLPKKVFEAAVKSIKAASSTEKFPDGFWLGEQLVCWQAG
                     TTPWNIFPVISLYLMGEVTNQSFRITILPQQYLRPVEDVATSQDDCYKFAVSQSSTGT
                     VMGAVIMEGFYVVFDRARKRIGFAVSACHVHDEFRTAAVEGPFVTADMEDCGYNIPQT
                     DESTLMTIAYVMAAICALFMLPLCLMVCQWRCLRCLRHQHDDFADDISLLK"
ORIGIN

Alignment Scores:
Pred. No.:              4.9e-12         Length:         4046
Score:                  143.00          Matches:        27
Percent Similarity:     100.00%         Conservative:   1
Best Local Similarity:  96.43%          Mismatches:     0
Query Match:            99.31%          Indels:         0
DB:                     3               Gaps:           0

US-10-726-967A-52 (1-28) x AK049626 (1-4046)

Qy          1 GlyTyrTyrValGluMetThrValGlySerProProGlnThrLeuAsnIleLeuValAsp 20
              ||||||||||||||||||||:::||||||||||||||||||||||||||||||||||||
Db        652 GGCTACTATGTGGAGATGACCATAGGCAGCCCCCCACAGACGCTCAACATCCTGGTGGAC 711

Qy         21 ThrGlySerSerAsnPheAlaVal 28
              |||||||||||||||||||||||||
Db        712 ACGGGCAGTAGTAACTTTGCAGTG 735

RESULT 14
AL700831
LOCUS       AL700831                461 bp    mRNA    linear   EST 04-SEP-2003
DEFINITION  DKFZp686I2411_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
            DKFZp686I2411 5', mRNA sequence.
ACCESSION   AL700831
VERSION     AL700831.1  GI:19621364
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 461)
  AUTHORS   Bloecker,H., Boecher,M., Brandt,P., Mewes,W., Weil,B. and
            Wiemann,S.
  TITLE     EST (Bloecker,H., Boecher,M., Brandt,P., Mewes,H.W., Weil,B. and
            Wiemann,S.)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: MIPS
            MIPS
            Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
            This is the 5' sequence of the clone insert
            Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de;
            sequenced by GBF (National Research Centre for Biotechnology Ltd.,
            Braunschweig/Germany) within the cDNA sequencing consortium of the
            German Genome Project.
            No s1 sequence available.
            This clone (DKFZp686I2411) is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES             Location/Qualifiers
     source          1. .461
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="DKFZp686I2411"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /clone_lib="686 (synonym: hlcc3)"
                     /note="Vector: pTriplEx2; Site_1: SfiIA; Site_2: SfiIB;
                     cDNA-collection"
ORIGIN

Alignment Scores:
Pred. No.:              2.36e-12        Length:         461
Score:                  138.00          Matches:        27
Percent Similarity:     96.43%          Conservative:   0
Best Local Similarity:  96.43%          Mismatches:     1
Query Match:            95.83%          Indels:         0
DB:                     1               Gaps:           0

US-10-726-967A-52 (1-28) x AL700831 (1-461)

Qy          1 GlyTyrTyrValGluMetThrValGlySerProProGlnThrLeuAsnIleLeuValAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         70 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGAT 129

Qy         21 ThrGlySerSerAsnPheAlaVal 28
              |||||||||  ||||||||||||
Db        130 ACAGGCAGCATTAACTTCGCAGTG 153

RESULT 15
BG288435
LOCUS       BG288435                720 bp    mRNA    linear   EST 11-JAN-2002
DEFINITION  602383404F1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:4500913 5',
            mRNA sequence.
ACCESSION   BG288435
VERSION     BG288435.1  GI:13043475
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 720)
```

AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10367 row: h column: 02
High quality sequence start: 8
High quality sequence stop: 715.
FEATURES Location/Qualifiers
source 1. .720
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:4500913"
/tissue_type="retina"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_94"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 3.3 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."
ORIGIN

Alignment Scores:

Pred. No.:	4.05e-12	Length:	720
Score:	138.00	Matches:	27
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	95.83%	Indels:	0
DB:	4	Gaps:	0

US-10-726-967A-52 (1-28) x BG288435 (1-720)

```
Qy          2 TyrTyrValGluMetThrValGlySerProProGlnThrLeuAsnIleLeuValAspThr 21
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          8 TACTATGTGGAGATGACCGTAGGCAGCCCCCCACAGACGCTCAACATCCTGGTGGACACG 67

Qy         22 GlySerSerAsnPheAlaVal 28
              ||||||||||||||||||||
Db         68 GGCAGTAGTAACTTTGCAGTG 88
```

Search completed: July 27, 2005, 18:17:56
Job time : 3160 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: July 26, 2005, 16:38:55 ; Search time 41 Seconds
(without alignments)
50.980 Million cell updates/sec

Title: US-10-726-967A-52
Perfect score: 144
Sequence: 1 GYYVEMTVGSPPQTLNILVDTGSSNFAV 28

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	144	100.0	231	4	US-09-471-669A-107	Sequence 107, App
2	144	100.0	361	4	US-09-724-566A-75	Sequence 75, Appl
3	144	100.0	361	4	US-09-471-669A-75	Sequence 75, Appl
4	144	100.0	374	4	US-09-724-566A-71	Sequence 71, Appl
5	144	100.0	374	4	US-09-471-669A-71	Sequence 71, Appl
6	144	100.0	380	4	US-09-471-669A-108	Sequence 108, App
7	144	100.0	390	4	US-09-724-566A-70	Sequence 70, Appl
8	144	100.0	390	4	US-09-471-669A-70	Sequence 70, Appl
9	144	100.0	395	4	US-09-724-566A-68	Sequence 68, Appl
10	144	100.0	395	4	US-09-471-669A-68	Sequence 68, Appl
11	144	100.0	401	4	US-09-471-669A-106	Sequence 106, App
12	144	100.0	407	4	US-09-724-566A-58	Sequence 58, Appl
13	144	100.0	407	4	US-09-471-669A-58	Sequence 58, Appl
14	144	100.0	408	4	US-09-471-669A-105	Sequence 105, App
15	144	100.0	419	4	US-09-724-566A-57	Sequence 57, Appl
16	144	100.0	419	4	US-09-471-669A-57	Sequence 57, Appl
17	144	100.0	420	4	US-09-724-566A-60	Sequence 60, Appl
18	144	100.0	420	4	US-09-471-669A-60	Sequence 60, Appl
19	144	100.0	425	4	US-09-548-372D-28	Sequence 28, Appl
20	144	100.0	425	4	US-09-548-367D-28	Sequence 28, Appl
21	144	100.0	425	4	US-09-551-853D-28	Sequence 28, Appl
22	144	100.0	425	4	US-09-416-901B-28	Sequence 28, Appl
23	144	100.0	425	4	US-09-548-376D-28	Sequence 28, Appl
24	144	100.0	425	4	US-09-794-927A-28	Sequence 28, Appl
25	144	100.0	425	4	US-09-548-373D-28	Sequence 28, Appl
26	144	100.0	425	4	US-09-795-847B-28	Sequence 28, Appl
27	144	100.0	425	4	US-09-869-414-28	Sequence 28, Appl
28	144	100.0	425	4	US-09-548-366F-28	Sequence 28, Appl
29	144	100.0	425	4	US-09-548-368D-28	Sequence 28, Appl
30	144	100.0	425	4	US-09-794-925A-28	Sequence 28, Appl
31	144	100.0	425	4	US-09-806-194A-28	Sequence 28, Appl
32	144	100.0	427	4	US-09-471-669A-65	Sequence 65, Appl
33	144	100.0	428	4	US-09-548-372D-51	Sequence 51, Appl
34	144	100.0	428	4	US-09-548-367D-51	Sequence 51, Appl
35	144	100.0	428	4	US-09-551-853D-51	Sequence 51, Appl
36	144	100.0	428	4	US-09-416-901B-51	Sequence 51, Appl
37	144	100.0	428	4	US-09-548-376D-51	Sequence 51, Appl
38	144	100.0	428	4	US-09-794-927A-51	Sequence 51, Appl
39	144	100.0	428	4	US-09-548-373D-51	Sequence 51, Appl
40	144	100.0	428	4	US-09-795-847B-51	Sequence 51, Appl
41	144	100.0	428	4	US-09-869-414-51	Sequence 51, Appl
42	144	100.0	428	4	US-09-548-366F-51	Sequence 51, Appl
43	144	100.0	428	4	US-09-548-368D-51	Sequence 51, Appl
44	144	100.0	428	4	US-09-794-925A-51	Sequence 51, Appl
45	144	100.0	431	4	US-09-724-566A-74	Sequence 74, Appl

ALIGNMENTS

RESULT 1
US-09-471-669A-107
; Sequence 107, Application US/09471669A
; Patent No. 6830918
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Guriqbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, No. 6830918mand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; APPLICANT: Elan Pharmaceuticals, Inc.
; TITLE OF INVENTION: BETA-SECRETASE ENZYME COMPOSITIONS AND METHODS
; FILE REFERENCE: 015270-006430US
; CURRENT APPLICATION NUMBER: US/09/471,669A
; CURRENT FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: US 60/114,408
; PRIOR FILING DATE: 1998-12-31
; PRIOR APPLICATION NUMBER: US 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: US 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 107
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: pBS/MuImPain E17 Brain #17 construct
US-09-471-669A-107

Query Match 100.0%; Score 144; DB 4; Length 231;
Best Local Similarity 100.0%; Pred. No. 6.5e-14;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GYYVEMTVGSPPQTLNILVDTGSSNFAV 28
              ||||||||||||||||||||||||||||
Db         15 GYYVEMTVGSPPQTLNILVDTGSSNFAV 42
```

RESULT 2
US-09-724-566A-75
; Sequence 75, Application US/09724566A
; Patent No. 6627739

; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Guriqbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, No. 6627739mand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 228-US-NEWC2
; CURRENT APPLICATION NUMBER: US/09/724,566A
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 75
; LENGTH: 361
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-566A-75

Query Match 100.0%; Score 144; DB 4; Length 361;
Best Local Similarity 100.0%; Pred. No. 1.1e-13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYYVEMTVGSPPQTLNILVDTGSSNFAV 28
||||||||||||||||||||||||||||
Db 12 GYYVEMTVGSPPQTLNILVDTGSSNFAV 39

RESULT 3
US-09-471-669A-75
; Sequence 75, Application US/09471669A
; Patent No. 6830918
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Guriqbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, No. 6830918mand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; APPLICANT: Elan Pharmaceuticals, Inc.
; TITLE OF INVENTION: BETA-SECRETASE ENZYME COMPOSITIONS AND METHODS
; FILE REFERENCE: 015270-006430US
; CURRENT APPLICATION NUMBER: US/09/471,669A
; CURRENT FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: US 60/114,408
; PRIOR FILING DATE: 1998-12-31
; PRIOR APPLICATION NUMBER: US 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: US 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 75
; LENGTH: 361
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-471-669A-75

Query Match 100.0%; Score 144; DB 4; Length 361;
Best Local Similarity 100.0%; Pred. No. 1.1e-13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYYVEMTVGSPPQTLNILVDTGSSNFAV 28
||||||||||||||||||||||||||||
Db 12 GYYVEMTVGSPPQTLNILVDTGSSNFAV 39

RESULT 4
US-09-724-566A-71
; Sequence 71, Application US/09724566A
; Patent No. 6627739
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Guriqbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, No. 6627739mand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 228-US-NEWC2
; CURRENT APPLICATION NUMBER: US/09/724,566A
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 71
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-566A-71

Query Match 100.0%; Score 144; DB 4; Length 374;
Best Local Similarity 100.0%; Pred. No. 1.1e-13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYYVEMTVGSPPQTLNILVDTGSSNFAV 28
||||||||||||||||||||||||||||
Db 29 GYYVEMTVGSPPQTLNILVDTGSSNFAV 56

RESULT 5
US-09-471-669A-71
; Sequence 71, Application US/09471669A
; Patent No. 6830918
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Guriqbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, No. 6830918mand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; APPLICANT: Elan Pharmaceuticals, Inc.
; TITLE OF INVENTION: BETA-SECRETASE ENZYME COMPOSITIONS AND METHODS

```
;  FILE REFERENCE: 015270-006430US
;  CURRENT APPLICATION NUMBER: US/09/471,669A
;  CURRENT FILING DATE:  1999-12-24
;  PRIOR APPLICATION NUMBER: US 60/114,408
;  PRIOR FILING DATE: 1998-12-31
;  PRIOR APPLICATION NUMBER: US 60/119,571
;  PRIOR FILING DATE: 1999-02-10
;  PRIOR APPLICATION NUMBER: US 60/139,172
;  PRIOR FILING DATE: 1999-06-15
;  NUMBER OF SEQ ID NOS: 108
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 71
;   LENGTH: 374
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-471-669A-71

  Query Match             100.0%;  Score 144;  DB 4;  Length 374;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-13;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GYYVEMTVGSPPQTLNILVDTGSSNFAV 28
              ||||||||||||||||||||||||||||
Db         29 GYYVEMTVGSPPQTLNILVDTGSSNFAV 56


RESULT 6
US-09-471-669A-108
; Sequence 108, Application US/09471669A
; Patent No. 6830918
; GENERAL INFORMATION:
;  APPLICANT: Anderson, John P.
;  APPLICANT:  Basi, Guriqbal
;  APPLICANT:  Doane, Minh Tam
;  APPLICANT:  Frigon, No. 6830918mand
;  APPLICANT:  John, Varghese
;  APPLICANT:  Power, Michael
;  APPLICANT:  Sinha, Sukanto
;  APPLICANT:  Tatsuno, Gwen
;  APPLICANT:  Tung, Jay
;  APPLICANT:  Wang, Shuwen
;  APPLICANT:  McConlogue, Lisa
;  APPLICANT:  Elan Pharmaceuticals, Inc.
;  TITLE OF INVENTION: BETA-SECRETASE ENZYME COMPOSITIONS AND METHODS
;  FILE REFERENCE: 015270-006430US
;  CURRENT APPLICATION NUMBER: US/09/471,669A
;  CURRENT FILING DATE:  1999-12-24
;  PRIOR APPLICATION NUMBER: US 60/114,408
;  PRIOR FILING DATE: 1998-12-31
;  PRIOR APPLICATION NUMBER: US 60/119,571
;  PRIOR FILING DATE: 1999-02-10
;  PRIOR APPLICATION NUMBER: US 60/139,172
;  PRIOR FILING DATE: 1999-06-15
;  NUMBER OF SEQ ID NOS: 108
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 108
;   LENGTH: 380
;   TYPE: PRT
;   ORGANISM: Mus sp.
;   FEATURE:
;   OTHER INFORMATION: pBS/MuImPain E17 Brain#15 construct
US-09-471-669A-108

  Query Match             100.0%;  Score 144;  DB 4;  Length 380;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-13;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GYYVEMTVGSPPQTLNILVDTGSSNFAV 28
              ||||||||||||||||||||||||||||
Db         15 GYYVEMTVGSPPQTLNILVDTGSSNFAV 42


RESULT 7
US-09-724-566A-70
; Sequence 70, Application US/09724566A
; Patent No. 6627739
; GENERAL INFORMATION:
;  APPLICANT: Anderson, John P.
;  APPLICANT:  Basi, Guriqbal
;  APPLICANT:  Doane, Minh Tam
;  APPLICANT:  Frigon, No. 6627739mand
;  APPLICANT:  John, Varghese
;  APPLICANT:  Power, Michael
;  APPLICANT:  Sinha, Sukanto
;  APPLICANT:  Tatsuno, Gwen
;  APPLICANT:  Tung, Jay
;  APPLICANT:  Wang, Shuwen
;  APPLICANT:  McConlogue, Lisa
;  TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
;  TITLE OF INVENTION:  Methods
;  FILE REFERENCE: 228-US-NEWC2
;  CURRENT APPLICATION NUMBER: US/09/724,566A
;  CURRENT FILING DATE:  2000-11-28
;  PRIOR APPLICATION NUMBER: US 09/501,708
;  PRIOR FILING DATE: 2000-02-10
;  PRIOR APPLICATION NUMBER: 60/119,571
;  PRIOR FILING DATE: 1999-02-10
;  PRIOR APPLICATION NUMBER: 60/139,172
;  PRIOR FILING DATE: 1999-06-15
;  NUMBER OF SEQ ID NOS: 104
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 70
;   LENGTH: 390
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-724-566A-70

  Query Match             100.0%;  Score 144;  DB 4;  Length 390;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-13;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GYYVEMTVGSPPQTLNILVDTGSSNFAV 28
              ||||||||||||||||||||||||||||
Db         12 GYYVEMTVGSPPQTLNILVDTGSSNFAV 39


RESULT 8
US-09-471-669A-70
; Sequence 70, Application US/09471669A
; Patent No. 6830918
; GENERAL INFORMATION:
;  APPLICANT: Anderson, John P.
;  APPLICANT:  Basi, Guriqbal
;  APPLICANT:  Doane, Minh Tam
;  APPLICANT:  Frigon, No. 6830918mand
;  APPLICANT:  John, Varghese
;  APPLICANT:  Power, Michael
;  APPLICANT:  Sinha, Sukanto
;  APPLICANT:  Tatsuno, Gwen
;  APPLICANT:  Tung, Jay
;  APPLICANT:  Wang, Shuwen
;  APPLICANT:  McConlogue, Lisa
;  APPLICANT:  Elan Pharmaceuticals, Inc.
;  TITLE OF INVENTION: BETA-SECRETASE ENZYME COMPOSITIONS AND METHODS
;  FILE REFERENCE: 015270-006430US
;  CURRENT APPLICATION NUMBER: US/09/471,669A
;  CURRENT FILING DATE:  1999-12-24
;  PRIOR APPLICATION NUMBER: US 60/114,408
;  PRIOR FILING DATE: 1998-12-31
;  PRIOR APPLICATION NUMBER: US 60/119,571
;  PRIOR FILING DATE: 1999-02-10
;  PRIOR APPLICATION NUMBER: US 60/139,172
;  PRIOR FILING DATE: 1999-06-15
;  NUMBER OF SEQ ID NOS: 108
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 70
```

; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-471-669A-70

Query Match 100.0%; Score 144; DB 4; Length 390;
Best Local Similarity 100.0%; Pred. No. 1.2e-13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYYVEMTVGSPPQTLNILVDTGSSNFAV 28
||||||||||||||||||||||||||||
Db 12 GYYVEMTVGSPPQTLNILVDTGSSNFAV 39

RESULT 9
US-09-724-566A-68
; Sequence 68, Application US/09724566A
; Patent No. 6627739
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Guriqbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, No. 6627739mand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 228-US-NEWC2
; CURRENT APPLICATION NUMBER: US/09/724,566A
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 68
; LENGTH: 395
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-566A-68

Query Match 100.0%; Score 144; DB 4; Length 395;
Best Local Similarity 100.0%; Pred. No. 1.2e-13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYYVEMTVGSPPQTLNILVDTGSSNFAV 28
||||||||||||||||||||||||||||
Db 17 GYYVEMTVGSPPQTLNILVDTGSSNFAV 44

RESULT 10
US-09-471-669A-68
; Sequence 68, Application US/09471669A
; Patent No. 6830918
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Guriqbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, No. 6830918mand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; APPLICANT: Elan Pharmaceuticals, Inc.
; TITLE OF INVENTION: BETA-SECRETASE ENZYME COMPOSITIONS AND METHODS
; FILE REFERENCE: 015270-006430US
; CURRENT APPLICATION NUMBER: US/09/471,669A
; CURRENT FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: US 60/114,408
; PRIOR FILING DATE: 1998-12-31
; PRIOR APPLICATION NUMBER: US 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: US 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 68
; LENGTH: 395
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-471-669A-68

Query Match 100.0%; Score 144; DB 4; Length 395;
Best Local Similarity 100.0%; Pred. No. 1.2e-13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYYVEMTVGSPPQTLNILVDTGSSNFAV 28
||||||||||||||||||||||||||||
Db 17 GYYVEMTVGSPPQTLNILVDTGSSNFAV 44

RESULT 11
US-09-471-669A-106
; Sequence 106, Application US/09471669A
; Patent No. 6830918
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Guriqbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, No. 6830918mand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; APPLICANT: Elan Pharmaceuticals, Inc.
; TITLE OF INVENTION: BETA-SECRETASE ENZYME COMPOSITIONS AND METHODS
; FILE REFERENCE: 015270-006430US
; CURRENT APPLICATION NUMBER: US/09/471,669A
; CURRENT FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: US 60/114,408
; PRIOR FILING DATE: 1998-12-31
; PRIOR APPLICATION NUMBER: US 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: US 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 106
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: pBS/MuImPain E17 #14 construct
US-09-471-669A-106

Query Match 100.0%; Score 144; DB 4; Length 401;
Best Local Similarity 100.0%; Pred. No. 1.2e-13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYYVEMTVGSPPQTLNILVDTGSSNFAV 28
||||||||||||||||||||||||||||
Db 25 GYYVEMTVGSPPQTLNILVDTGSSNFAV 52

```
RESULT 12
US-09-724-566A-58
; Sequence 58, Application US/09724566A
; Patent No. 6627739
; GENERAL INFORMATION:
;  APPLICANT: Anderson, John P.
;  APPLICANT:  Basi, Guriqbal
;  APPLICANT:  Doane, Minh Tam
;  APPLICANT:  Frigon, No. 6627739mand
;  APPLICANT:  John, Varghese
;  APPLICANT:  Power, Michael
;  APPLICANT:  Sinha, Sukanto
;  APPLICANT:  Tatsuno, Gwen
;  APPLICANT:  Tung, Jay
;  APPLICANT:  Wang, Shuwen
;  APPLICANT:  McConlogue, Lisa
;  TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
;  TITLE OF INVENTION:  Methods
;  FILE REFERENCE: 228-US-NEWC2
;  CURRENT APPLICATION NUMBER: US/09/724,566A
;  CURRENT FILING DATE:  2000-11-28
;  PRIOR APPLICATION NUMBER: US 09/501,708
;  PRIOR FILING DATE: 2000-02-10
;  PRIOR APPLICATION NUMBER: 60/119,571
;  PRIOR FILING DATE: 1999-02-10
;  PRIOR APPLICATION NUMBER: 60/139,172
;  PRIOR FILING DATE: 1999-06-15
;  NUMBER OF SEQ ID NOS: 104
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 58
;   LENGTH: 407
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-724-566A-58

  Query Match             100.0%;  Score 144;  DB 4;  Length 407;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-13;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GYYVEMTVGSPPQTLNILVDTGSSNFAV 28
              ||||||||||||||||||||||||||||
Db         29 GYYVEMTVGSPPQTLNILVDTGSSNFAV 56


RESULT 13
US-09-471-669A-58
; Sequence 58, Application US/09471669A
; Patent No. 6830918
; GENERAL INFORMATION:
;  APPLICANT: Anderson, John P.
;  APPLICANT:  Basi, Guriqbal
;  APPLICANT:  Doane, Minh Tam
;  APPLICANT:  Frigon, No. 6830918mand
;  APPLICANT:  John, Varghese
;  APPLICANT:  Power, Michael
;  APPLICANT:  Sinha, Sukanto
;  APPLICANT:  Tatsuno, Gwen
;  APPLICANT:  Tung, Jay
;  APPLICANT:  Wang, Shuwen
;  APPLICANT:  McConlogue, Lisa
;  APPLICANT:  Elan Pharmaceuticals, Inc.
;  TITLE OF INVENTION: BETA-SECRETASE ENZYME COMPOSITIONS AND METHODS
;  FILE REFERENCE: 015270-006430US
;  CURRENT APPLICATION NUMBER: US/09/471,669A
;  CURRENT FILING DATE:  1999-12-24
;  PRIOR APPLICATION NUMBER: US 60/114,408
;  PRIOR FILING DATE: 1998-12-31
;  PRIOR APPLICATION NUMBER: US 60/119,571
;  PRIOR FILING DATE: 1999-02-10
;  PRIOR APPLICATION NUMBER: US 60/139,172
;  PRIOR FILING DATE: 1999-06-15
;  NUMBER OF SEQ ID NOS: 108
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 58
;   LENGTH: 407
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-471-669A-58

  Query Match             100.0%;  Score 144;  DB 4;  Length 407;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-13;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GYYVEMTVGSPPQTLNILVDTGSSNFAV 28
              ||||||||||||||||||||||||||||
Db         29 GYYVEMTVGSPPQTLNILVDTGSSNFAV 56


RESULT 14
US-09-471-669A-105
; Sequence 105, Application US/09471669A
; Patent No. 6830918
; GENERAL INFORMATION:
;  APPLICANT: Anderson, John P.
;  APPLICANT:  Basi, Guriqbal
;  APPLICANT:  Doane, Minh Tam
;  APPLICANT:  Frigon, No. 6830918mand
;  APPLICANT:  John, Varghese
;  APPLICANT:  Power, Michael
;  APPLICANT:  Sinha, Sukanto
;  APPLICANT:  Tatsuno, Gwen
;  APPLICANT:  Tung, Jay
;  APPLICANT:  Wang, Shuwen
;  APPLICANT:  McConlogue, Lisa
;  APPLICANT:  Elan Pharmaceuticals, Inc.
;  TITLE OF INVENTION: BETA-SECRETASE ENZYME COMPOSITIONS AND METHODS
;  FILE REFERENCE: 015270-006430US
;  CURRENT APPLICATION NUMBER: US/09/471,669A
;  CURRENT FILING DATE:  1999-12-24
;  PRIOR APPLICATION NUMBER: US 60/114,408
;  PRIOR FILING DATE: 1998-12-31
;  PRIOR APPLICATION NUMBER: US 60/119,571
;  PRIOR FILING DATE: 1999-02-10
;  PRIOR APPLICATION NUMBER: US 60/139,172
;  PRIOR FILING DATE: 1999-06-15
;  NUMBER OF SEQ ID NOS: 108
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 105
;   LENGTH: 408
;   TYPE: PRT
;   ORGANISM: Mus sp.
;   FEATURE:
;   OTHER INFORMATION: pBS/MuImPain E17 #11 construct
US-09-471-669A-105

  Query Match             100.0%;  Score 144;  DB 4;  Length 408;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-13;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GYYVEMTVGSPPQTLNILVDTGSSNFAV 28
              ||||||||||||||||||||||||||||
Db         27 GYYVEMTVGSPPQTLNILVDTGSSNFAV 54


RESULT 15
US-09-724-566A-57
; Sequence 57, Application US/09724566A
; Patent No. 6627739
; GENERAL INFORMATION:
;  APPLICANT: Anderson, John P.
;  APPLICANT:  Basi, Guriqbal
;  APPLICANT:  Doane, Minh Tam
;  APPLICANT:  Frigon, No. 6627739mand
;  APPLICANT:  John, Varghese
```

```
;  APPLICANT:  Power, Michael
;  APPLICANT:  Sinha, Sukanto
;  APPLICANT:  Tatsuno, Gwen
;  APPLICANT:  Tung, Jay
;  APPLICANT:  Wang, Shuwen
;  APPLICANT:  McConlogue, Lisa
;  TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
;  TITLE OF INVENTION:  Methods
;  FILE REFERENCE: 228-US-NEWC2
;  CURRENT APPLICATION NUMBER: US/09/724,566A
;  CURRENT FILING DATE:  2000-11-28
;  PRIOR APPLICATION NUMBER: US 09/501,708
;  PRIOR FILING DATE: 2000-02-10
;  PRIOR APPLICATION NUMBER: 60/119,571
;  PRIOR FILING DATE: 1999-02-10
;  PRIOR APPLICATION NUMBER: 60/139,172
;  PRIOR FILING DATE: 1999-06-15
;  NUMBER OF SEQ ID NOS: 104
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 57
;   LENGTH: 419
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-724-566A-57

  Query Match             100.0%;  Score 144;  DB 4;  Length 419;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-13;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GYYVEMTVGSPPQTLNILVDTGSSNFAV 28
              ||||||||||||||||||||||||||||
Db         74 GYYVEMTVGSPPQTLNILVDTGSSNFAV 101


Search completed: July 26, 2005, 16:48:45
Job time : 41 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: July 26, 2005, 16:41:36 ; Search time 154 Seconds
(without alignments)
70.726 Million cell updates/sec

Title: US-10-726-967A-52
Perfect score: 144
Sequence: 1 GYYVEMTVGSPPQTLNILVDTGSSNFAV 28

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1741741 seqs, 388992284 residues

Total number of hits satisfying chosen parameters: 1741741

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep:*
20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	144	100.0	28	17	US-10-726-967A-52	Sequence 52, Appl
2	144	100.0	358	17	US-10-872-198-12	Sequence 12, Appl
3	144	100.0	358	17	US-10-872-197A-12	Sequence 12, Appl
4	144	100.0	391	15	US-10-372-473-4	Sequence 4, Appli
5	144	100.0	403	15	US-10-400-273-4	Sequence 4, Appli
6	144	100.0	406	16	US-10-837-021A-2	Sequence 2, Appli
7	144	100.0	406	16	US-10-837-021A-3	Sequence 3, Appli
8	144	100.0	406	16	US-10-837-021A-4	Sequence 4, Appli
9	144	100.0	406	16	US-10-837-021A-5	Sequence 5, Appli
10	144	100.0	408	15	US-10-400-273-5	Sequence 5, Appli
11	144	100.0	411	15	US-10-400-273-1	Sequence 1, Appli
12	144	100.0	411	15	US-10-627-473-19	Sequence 19, Appl
13	144	100.0	411	15	US-10-627-473-20	Sequence 20, Appl
14	144	100.0	414	16	US-10-281-092-9	Sequence 9, Appli
15	144	100.0	417	15	US-10-627-473-21	Sequence 21, Appl
16	144	100.0	425	9	US-09-794-927-28	Sequence 28, Appl
17	144	100.0	425	9	US-09-795-847-28	Sequence 28, Appl
18	144	100.0	425	9	US-09-794-743-28	Sequence 28, Appl
19	144	100.0	425	9	US-09-794-748-28	Sequence 28, Appl
20	144	100.0	425	9	US-09-794-925-28	Sequence 28, Appl
21	144	100.0	425	9	US-09-681-442-28	Sequence 28, Appl
22	144	100.0	425	10	US-09-869-414-28	Sequence 28, Appl
23	144	100.0	425	10	US-09-548-366-28	Sequence 28, Appl
24	144	100.0	425	15	US-10-372-473-3	Sequence 3, Appli
25	144	100.0	425	15	US-10-652-927-28	Sequence 28, Appl
26	144	100.0	425	15	US-10-652-830-28	Sequence 28, Appl
27	144	100.0	425	16	US-10-652-045-28	Sequence 28, Appl
28	144	100.0	425	16	US-10-476-935-28	Sequence 28, Appl
29	144	100.0	425	17	US-10-940-867-28	Sequence 28, Appl
30	144	100.0	425	17	US-10-477-076-28	Sequence 28, Appl
31	144	100.0	428	9	US-09-794-927-51	Sequence 51, Appl
32	144	100.0	428	9	US-09-795-847-51	Sequence 51, Appl
33	144	100.0	428	9	US-09-794-743-51	Sequence 51, Appl
34	144	100.0	428	9	US-09-794-748-51	Sequence 51, Appl
35	144	100.0	428	9	US-09-794-925-51	Sequence 51, Appl
36	144	100.0	428	9	US-09-681-442-51	Sequence 51, Appl
37	144	100.0	428	10	US-09-869-414-51	Sequence 51, Appl
38	144	100.0	428	10	US-09-548-366-51	Sequence 51, Appl
39	144	100.0	428	15	US-10-652-927-51	Sequence 51, Appl
40	144	100.0	428	15	US-10-652-830-51	Sequence 51, Appl
41	144	100.0	428	16	US-10-652-045-51	Sequence 51, Appl
42	144	100.0	428	16	US-10-476-935-51	Sequence 51, Appl
43	144	100.0	428	17	US-10-477-076-51	Sequence 51, Appl
44	144	100.0	432	15	US-10-372-473-2	Sequence 2, Appli
45	144	100.0	433	9	US-09-794-927-26	Sequence 26, Appl

ALIGNMENTS

RESULT 1
US-10-726-967A-52
; Sequence 52, Application US/10726967A
; Publication No. US20050074456A1
; GENERAL INFORMATION:
; APPLICANT: Ballinger, Marcus
; TITLE OF INVENTION: Constructs for Homogenously Processed Preparations of Beta Site
; TITLE OF INVENTION: App-Cleaving Enzyme
; FILE REFERENCE: 2004345-0021
; CURRENT APPLICATION NUMBER: US/10/726,967A
; CURRENT FILING DATE: 2003-12-02
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 52
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Residues 74-101 of human BACE1 preprosequence
US-10-726-967A-52

Query Match 100.0%; Score 144; DB 17; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.8e-14;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GYYVEMTVGSPPQTLNILVDTGSSNFAV 28
              ||||||||||||||||||||||||||||
Db          1 GYYVEMTVGSPPQTLNILVDTGSSNFAV 28
```

RESULT 2
US-10-872-198-12
; Sequence 12, Application US/10872198
; Publication No. US20050002897A1

; GENERAL INFORMATION:
; APPLICANT: Ulrich HAUPTS
; APPLICANT: Andre KOLTERMANN
; APPLICANT: Andreas SCHEIDIG
; APPLICANT: Christian VOETSMEIER
; APPLICANT: Ulrich Kettling
; TITLE OF INVENTION: NEW BIOLOGICAL ENTITIES AND USE THEREOF
; FILE REFERENCE: 04156.0002U4
; CURRENT APPLICATION NUMBER: US/10/872,198
; CURRENT FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 60/543,518
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/524,960
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: EP 04003058
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: EP 03025871
; PRIOR FILING DATE: 2003-11-11
; PRIOR APPLICATION NUMBER: EP 03025851
; PRIOR FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: EP 03013819
; PRIOR FILING DATE: 2003-06-18
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-872-198-12

Query Match 100.0%; Score 144; DB 17; Length 358;
Best Local Similarity 100.0%; Pred. No. 3.5e-13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYYVEMTVGSPPQTLNILVDTGSSNFAV 28
||||||||||||||||||||||||||||
Db 13 GYYVEMTVGSPPQTLNILVDTGSSNFAV 40

RESULT 3
US-10-872-197A-12
; Sequence 12, Application US/10872197A
; Publication No. US20050059126A1
; GENERAL INFORMATION:
; APPLICANT: Ulrich HAUPTS
; APPLICANT: Andre KOLTERMANN
; APPLICANT: Andreas SCHEIDIG
; APPLICANT: Christian VOTSMEIER
; APPLICANT: Ulrich KETTLING
; TITLE OF INVENTION: NEW BIOLOGICAL ENTITIES AND USE THEREOF
; FILE REFERENCE: 04156.0002U3
; CURRENT APPLICATION NUMBER: US/10/872,197A
; CURRENT FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 60/524,960
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: EP 03025871
; PRIOR FILING DATE: 2003-11-11
; PRIOR APPLICATION NUMBER: EP 03013819
; PRIOR FILING DATE: 2003-11-10
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-872-197A-12

Query Match 100.0%; Score 144; DB 17; Length 358;
Best Local Similarity 100.0%; Pred. No. 3.5e-13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYYVEMTVGSPPQTLNILVDTGSSNFAV 28
||||||||||||||||||||||||||||
Db 13 GYYVEMTVGSPPQTLNILVDTGSSNFAV 40

RESULT 4
US-10-372-473-4
; Sequence 4, Application US/10372473
; Publication No. US20040005691A1
; GENERAL INFORMATION:
; APPLICANT: Chou, Kuo-Chen
; APPLICANT: Howe, W. Jeffery
; TITLE OF INVENTION: Modified BACE
; FILE REFERENCE: MBHB 01-1766-A
; CURRENT APPLICATION NUMBER: US/10/372,473
; CURRENT FILING DATE: 2003-02-21
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; OTHER INFORMATION: Human beta-secretase.
US-10-372-473-4

Query Match 100.0%; Score 144; DB 15; Length 391;
Best Local Similarity 100.0%; Pred. No. 3.9e-13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYYVEMTVGSPPQTLNILVDTGSSNFAV 28
||||||||||||||||||||||||||||
Db 19 GYYVEMTVGSPPQTLNILVDTGSSNFAV 46

RESULT 5
US-10-400-273-4
; Sequence 4, Application US/10400273
; Publication No. US20040014194A1
; GENERAL INFORMATION:
; APPLICANT: Beyer, Brian
; APPLICANT: Hammond, Gerald S
; APPLICANT: Reichert, Paul
; APPLICANT: Strickland, Corey
; APPLICANT: Wang, Wenyan
; APPLICANT: Weber, Patricia C
; APPLICANT: Wong, Gwendolyn
; APPLICANT: Zhang, Lili
; TITLE OF INVENTION: BETA-SECRETASE CRYSTALS AND METHODS FOR PREPARING AND USING THE S.
; FILE REFERENCE: JB01531-K-US
; CURRENT APPLICATION NUMBER: US/10/400,273
; CURRENT FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: 60/367,937
; PRIOR FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-400-273-4

Query Match 100.0%; Score 144; DB 15; Length 403;
Best Local Similarity 100.0%; Pred. No. 4e-13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYYVEMTVGSPPQTLNILVDTGSSNFAV 28
||||||||||||||||||||||||||||
Db 27 GYYVEMTVGSPPQTLNILVDTGSSNFAV 54

RESULT 6
US-10-837-021A-2
; Sequence 2, Application US/10837021A

; Publication No. US20040265965A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P
; APPLICANT: McConlogue, Lisa
; APPLICANT: Basi, Guriqbal
; APPLICANT: Sinha, Sukatno
; TITLE OF INVENTION: Glycosylation Variants of BACE
; FILE REFERENCE: MBHB-03-268-A
; CURRENT APPLICATION NUMBER: US/10/837,021A
; CURRENT FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: 60/467,509
; PRIOR FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Human BACE with asparagine to alanine (N223A) mutation.
US-10-837-021A-2

Query Match 100.0%; Score 144; DB 16; Length 406;
Best Local Similarity 100.0%; Pred. No. 4e-13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYYVEMTVGSPPQTLNILVDTGSSNFAV 28
||||||||||||||||||||||||||||
Db 29 GYYVEMTVGSPPQTLNILVDTGSSNFAV 56

RESULT 7
US-10-837-021A-3
; Sequence 3, Application US/10837021A
; Publication No. US20040265965A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P
; APPLICANT: McConlogue, Lisa
; APPLICANT: Basi, Guriqbal
; APPLICANT: Sinha, Sukatno
; TITLE OF INVENTION: Glycosylation Variants of BACE
; FILE REFERENCE: MBHB-03-268-A
; CURRENT APPLICATION NUMBER: US/10/837,021A
; CURRENT FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: 60/467,509
; PRIOR FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Human BACE with serine to isoleucine (S174I) and asparagine to
; OTHER INFORMATION: alanine (N223A) mutations.
US-10-837-021A-3

Query Match 100.0%; Score 144; DB 16; Length 406;
Best Local Similarity 100.0%; Pred. No. 4e-13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYYVEMTVGSPPQTLNILVDTGSSNFAV 28
||||||||||||||||||||||||||||
Db 29 GYYVEMTVGSPPQTLNILVDTGSSNFAV 56

RESULT 8
US-10-837-021A-4
; Sequence 4, Application US/10837021A
; Publication No. US20040265965A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P
; APPLICANT: McConlogue, Lisa
; APPLICANT: Basi, Guriqbal
; APPLICANT: Sinha, Sukatno
; TITLE OF INVENTION: Glycosylation Variants of BACE
; FILE REFERENCE: MBHB-03-268-A
; CURRENT APPLICATION NUMBER: US/10/837,021A
; CURRENT FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: 60/467,509
; PRIOR FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Human BACE with serine to isoleucine (S174I), asparagine to
; OTHER INFORMATION: glutamine (N153Q) and asparagine to alanine (N223A) mutations.
US-10-837-021A-4

Query Match 100.0%; Score 144; DB 16; Length 406;
Best Local Similarity 100.0%; Pred. No. 4e-13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYYVEMTVGSPPQTLNILVDTGSSNFAV 28
||||||||||||||||||||||||||||
Db 29 GYYVEMTVGSPPQTLNILVDTGSSNFAV 56

RESULT 9
US-10-837-021A-5
; Sequence 5, Application US/10837021A
; Publication No. US20040265965A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P
; APPLICANT: McConlogue, Lisa
; APPLICANT: Basi, Guriqbal
; APPLICANT: Sinha, Sukatno
; TITLE OF INVENTION: Glycosylation Variants of BACE
; FILE REFERENCE: MBHB-03-268-A
; CURRENT APPLICATION NUMBER: US/10/837,021A
; CURRENT FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: 60/467,509
; PRIOR FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Human BACE with serine to isoleucine (S174I), asparagine to
; OTHER INFORMATION: glutamine (N153Q), asparagine to alanine (N223A) and asparagine
; OTHER INFORMATION: to seine (N354S) mutations.
US-10-837-021A-5

Query Match 100.0%; Score 144; DB 16; Length 406;
Best Local Similarity 100.0%; Pred. No. 4e-13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYYVEMTVGSPPQTLNILVDTGSSNFAV 28
||||||||||||||||||||||||||||
Db 29 GYYVEMTVGSPPQTLNILVDTGSSNFAV 56

RESULT 10
US-10-400-273-5
; Sequence 5, Application US/10400273
; Publication No. US20040014194A1
; GENERAL INFORMATION:
; APPLICANT: Beyer, Brian
; APPLICANT: Hammond, Gerald S
; APPLICANT: Reichert, Paul
; APPLICANT: Strickland, Corey

```
;  APPLICANT:  Wang, Wenyan
;  APPLICANT:  Weber, Patricia C
;  APPLICANT:  Wong, Gwendolyn
;  APPLICANT:  Zhang, Lili
;  TITLE OF INVENTION: BETA-SECRETASE CRYSTALS AND METHODS FOR PREPARING AND USING THE S
;  FILE REFERENCE: JB01531-K-US
;  CURRENT APPLICATION NUMBER: US/10/400,273
;  CURRENT FILING DATE:  2003-03-26
;  PRIOR APPLICATION NUMBER: 60/367,937
;  PRIOR FILING DATE: 2002-03-27
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
;   LENGTH: 408
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-400-273-5

  Query Match             100.0%;  Score 144;  DB 15;  Length 408;
  Best Local Similarity   100.0%;  Pred. No. 4.1e-13;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GYYVEMTVGSPPQTLNILVDTGSSNFAV 28
              ||||||||||||||||||||||||||||
Db         32 GYYVEMTVGSPPQTLNILVDTGSSNFAV 59


RESULT 11
US-10-400-273-1
; Sequence 1, Application US/10400273
; Publication No. US20040014194A1
; GENERAL INFORMATION:
;  APPLICANT: Beyer, Brian
;  APPLICANT:  Hammond, Gerald S
;  APPLICANT:  Reichert, Paul
;  APPLICANT:  Strickland, Corey
;  APPLICANT:  Wang, Wenyan
;  APPLICANT:  Weber, Patricia C
;  APPLICANT:  Wong, Gwendolyn
;  APPLICANT:  Zhang, Lili
;  TITLE OF INVENTION: BETA-SECRETASE CRYSTALS AND METHODS FOR PREPARING AND USING THE S
;  FILE REFERENCE: JB01531-K-US
;  CURRENT APPLICATION NUMBER: US/10/400,273
;  CURRENT FILING DATE:  2003-03-26
;  PRIOR APPLICATION NUMBER: 60/367,937
;  PRIOR FILING DATE: 2002-03-27
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 411
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-400-273-1

  Query Match             100.0%;  Score 144;  DB 15;  Length 411;
  Best Local Similarity   100.0%;  Pred. No. 4.1e-13;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GYYVEMTVGSPPQTLNILVDTGSSNFAV 28
              ||||||||||||||||||||||||||||
Db         29 GYYVEMTVGSPPQTLNILVDTGSSNFAV 56


RESULT 12
US-10-627-473-19
; Sequence 19, Application US/10627473
; Publication No. US20040096950A1
; GENERAL INFORMATION:
;  APPLICANT: VUILLARD, LAURENT MICHEL MARIE
;  APPLICANT:  PATEL, SAHIL JOE
;  APPLICANT:  YON, JEFFREY ROLAND
;  APPLICANT:  CLEASBY, ANNE
;  APPLICANT:  HAMILTON, BRUCE JOHN
;  APPLICANT:  SHAH, ALEEM
;  TITLE OF INVENTION: CRYSTAL STRUCTURE OF BETA SITE APP CLEAVING ENZYME
;  TITLE OF INVENTION:  (BACE) AND METHODS OF USE THEREOF
;  FILE REFERENCE: 674553-2002.1
;  CURRENT APPLICATION NUMBER: US/10/627,473
;  CURRENT FILING DATE:  2003-07-25
;  PRIOR APPLICATION NUMBER: 60/398,681
;  PRIOR FILING DATE: 2002-07-26
;  NUMBER OF SEQ ID NOS: 46
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
;   LENGTH: 411
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-627-473-19

  Query Match             100.0%;  Score 144;  DB 15;  Length 411;
  Best Local Similarity   100.0%;  Pred. No. 4.1e-13;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GYYVEMTVGSPPQTLNILVDTGSSNFAV 28
              ||||||||||||||||||||||||||||
Db         32 GYYVEMTVGSPPQTLNILVDTGSSNFAV 59


RESULT 13
US-10-627-473-20
; Sequence 20, Application US/10627473
; Publication No. US20040096950A1
; GENERAL INFORMATION:
;  APPLICANT: VUILLARD, LAURENT MICHEL MARIE
;  APPLICANT:  PATEL, SAHIL JOE
;  APPLICANT:  YON, JEFFREY ROLAND
;  APPLICANT:  CLEASBY, ANNE
;  APPLICANT:  HAMILTON, BRUCE JOHN
;  APPLICANT:  SHAH, ALEEM
;  TITLE OF INVENTION: CRYSTAL STRUCTURE OF BETA SITE APP CLEAVING ENZYME
;  TITLE OF INVENTION:  (BACE) AND METHODS OF USE THEREOF
;  FILE REFERENCE: 674553-2002.1
;  CURRENT APPLICATION NUMBER: US/10/627,473
;  CURRENT FILING DATE:  2003-07-25
;  PRIOR APPLICATION NUMBER: 60/398,681
;  PRIOR FILING DATE: 2002-07-26
;  NUMBER OF SEQ ID NOS: 46
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
;   LENGTH: 411
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-627-473-20

  Query Match             100.0%;  Score 144;  DB 15;  Length 411;
  Best Local Similarity   100.0%;  Pred. No. 4.1e-13;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GYYVEMTVGSPPQTLNILVDTGSSNFAV 28
              ||||||||||||||||||||||||||||
Db         32 GYYVEMTVGSPPQTLNILVDTGSSNFAV 59


RESULT 14
US-10-281-092-9
; Sequence 9, Application US/10281092
; Publication No. US20040121947A1
; GENERAL INFORMATION:
;  APPLICANT: Ghosh, Arun K.
;  APPLICANT:  Tang, Jordan J.N.
;  APPLICANT:  Bilcer, Geoffrey
;  APPLICANT:  Chang, Wanpin
;  APPLICANT:  Hong, Lin
;  APPLICANT:  Koelsch, Gerald E.
;  APPLICANT:  Loy, Jeffrey A.
;  APPLICANT:  Turner, Robert T., III
```

; APPLICANT: Devasumadrum, Thippeswamy
; TITLE OF INVENTION: COMPOUNDS WHICH INHIBIT BETA-SECRETASE
; TITLE OF INVENTION: ACTIVITY AND METHODS OF USE THEREOF
; FILE REFERENCE: 2932.1001-004
; CURRENT APPLICATION NUMBER: US/10/281,092
; CURRENT FILING DATE: 2002-10-23
; PRIOR APPLICATION NUMBER: US 10/032,818
; PRIOR FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: PCT US01/50826
; PRIOR FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: US 60/258,705
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 60/275,756
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: US 60/335,952
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: US 60/333,545
; PRIOR FILING DATE: 2001-11-27
; PRIOR APPLICATION NUMBER: US 60/348,464
; PRIOR FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/348,615
; PRIOR FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/390,804
; PRIOR FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: US 60/397,557
; PRIOR FILING DATE: 2002-07-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 414
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: memapsin 2
US-10-281-092-9

Query Match 100.0%; Score 144; DB 16; Length 414;
Best Local Similarity 100.0%; Pred. No. 4.1e-13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYYVEMTVGSPPQTLNILVDTGSSNFAV 28
||||||||||||||||||||||||||||
Db 34 GYYVEMTVGSPPQTLNILVDTGSSNFAV 61

RESULT 15
US-10-627-473-21
; Sequence 21, Application US/10627473
; Publication No. US20040096950A1
; GENERAL INFORMATION:
; APPLICANT: VUILLARD, LAURENT MICHEL MARIE
; APPLICANT: PATEL, SAHIL JOE
; APPLICANT: YON, JEFFREY ROLAND
; APPLICANT: CLEASBY, ANNE
; APPLICANT: HAMILTON, BRUCE JOHN
; APPLICANT: SHAH, ALEEM
; TITLE OF INVENTION: CRYSTAL STRUCTURE OF BETA SITE APP CLEAVING ENZYME
; TITLE OF INVENTION: (BACE) AND METHODS OF USE THEREOF
; FILE REFERENCE: 674553-2002.1
; CURRENT APPLICATION NUMBER: US/10/627,473
; CURRENT FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: 60/398,681
; PRIOR FILING DATE: 2002-07-26
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-627-473-21

Query Match 100.0%; Score 144; DB 15; Length 417;
Best Local Similarity 100.0%; Pred. No. 4.2e-13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYYVEMTVGSPPQTLNILVDTGSSNFAV 28
||||||||||||||||||||||||||||
Db 32 GYYVEMTVGSPPQTLNILVDTGSSNFAV 59

Search completed: July 26, 2005, 16:51:25
Job time : 154 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: July 26, 2005, 16:38:10 ; Search time 39 Seconds
(without alignments)
69.079 Million cell updates/sec

Title: US-10-726-967A-52
Perfect score: 144
Sequence: 1 GYYVEMTVGSPPQTLNILVDTGSSNFAV 28

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	144	100.0	501	2	A59090	aspartic proteinas
2	91	63.2	709	2	T29692	hypothetical prote
3	90	62.5	396	2	T47207	aspartic proteinas
4	87	60.4	405	2	A25379	saccharopepsin (EC
5	83	57.6	398	2	T33383	hypothetical prote
6	83	57.6	406	1	REHUK	renin (EC 3.4.23.1
7	82	56.9	383	2	JC7573	pepsinogen C - Afr
8	82	56.9	384	2	A39314	gastricsin (EC 3.4
9	82	56.9	389	2	JE0371	pepsin C (EC 3.4.2
10	82	56.9	400	2	I47099	renin (EC 3.4.23.1
11	82	56.9	401	1	REMSS	renin (EC 3.4.23.1
12	82	56.9	402	1	REMSK	renin (EC 3.4.23.1
13	82	56.9	506	2	S71591	aspartic proteinas
14	82	56.9	508	2	D85056	probable aspartic
15	82	56.9	509	2	S49349	cyprosin (EC 3.4.2
16	82	56.9	596	2	S57971	aspartic proteinas
17	81	56.2	387	2	A45117	aspartic proteinas
18	81	56.2	433	2	E96649	hypothetical prote
19	81	56.2	513	2	T09739	aspartic endopepti
20	81	56.2	537	2	S50344	aspergillopepsin h
21	80	55.6	506	2	F86253	hypothetical prote
22	80	55.6	506	2	T07915	probable aspartic
23	80	55.6	569	2	S64957	aspergillopepsin I
24	79	54.9	375	2	C96715	protein F4N2.8 [im
25	78	54.2	165	2	S61602	probable membrane
26	78	54.2	344	1	KHPGD	cathepsin D (EC 3.
27	78	54.2	377	1	PEMQCJ	gastricsin (EC 3.4
28	78	54.2	388	2	JC7246	pepsinogen C - com
29	78	54.2	388	2	A29937	gastricsin (EC 3.4
30	78	54.2	392	1	A24608	gastricsin (EC 3.4
31	78	54.2	398	2	I51185	cathepsin D (EC 3.
32	78	54.2	407	1	KHRTD	cathepsin D (EC 3.
33	78	54.2	412	1	KHHUD	cathepsin D (EC 3.
34	77	53.5	394	2	B43356	gastricsin (EC 3.4
35	76	52.8	391	2	A43356	cathepsin E (EC 3.
36	76	52.8	396	2	A34401	cathepsin E (EC 3.
37	76	52.8	508	2	S19697	aspartic proteinas
38	76	52.8	509	2	S66516	oryzasin (EC 3.4.2
39	75	52.1	383	2	A41443	pepsin (EC 3.4.23.
40	75	52.1	410	1	KHMSD	cathepsin D (EC 3.
41	75	52.1	428	2	S47096	cynarase (EC 3.4.2
42	75	52.1	435	2	T45035	hypothetical prote
43	75	52.1	474	2	T12049	cyprosin (EC 3.4.2
44	74	51.4	151	2	T18478	hypothetical prote
45	74	51.4	189	2	T18480	hypothetical prote

ALIGNMENTS

RESULT 1
A59090
aspartic proteinase (EC 3.4.23.-) BACE precursor - human
N;Alternate names: beta-secretase; beta-site APP cleaving enzyme
C;Species: Homo sapiens (man)
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: A59090
R;Vassar, R.; Bennett, B.D.; Babu-Khan, S.; Kahn, S.; Mendiaz, E.A.; Denis, P.; Teplow, M.A.; Biere, A.L.; Curran, E.; Burgess, T.; Louis, J.C.; Collins, F.; Treanor, J.; Roge
Science 286, 735-741, 1999
A;Title: beta-Secretase cleavage of Alzheimer's amyloid precursor protein by the transm
A;Reference number: A59090; MUID:20002972; PMID:10531052
A;Note: submitted to GenBank, September 1999
A;Accession: A59090
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-501 <VAS>
A;Cross-references: UNIPROT:P56817; GB:AF190725; NID:g6118538; PIDN:AAF04142.1; PID:g61
C;Genetics:
A;Gene: BACE
C;Superfamily: beta-secretase
C;Keywords: Alzheimer's disease; aspartic proteinase; brain; glycoprotein; hydrolase; p
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-45/Domain: propeptide #status predicted <PRO>
F;46-501/Product: acid proteinase BACE #status predicted <MAT>
F;461-477/Domain: transmembrane #status predicted <TRN>
F;93,289/Active site: Asp #status predicted
F;153,172,223,354/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;330-380/Disulfide bonds: #status predicted

Query Match 100.0%; Score 144; DB 2; Length 501;
Best Local Similarity 100.0%; Pred. No. 7.3e-14;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GYYVEMTVGSPPQTLNILVDTGSSNFAV 28
              ||||||||||||||||||||||||||||
Db         74 GYYVEMTVGSPPQTLNILVDTGSSNFAV 101
```

RESULT 2
T29692
hypothetical protein T18H9.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T29692
R;Du, Z.; Gattung, S.
submitted to the EMBL Data Library, November 1995
A;Description: The sequence of C. elegans cosmid T18H9.
A;Reference number: Z20666
A;Accession: T29692
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA

```
A;Residues: 1-709 <DUZ>
A;Cross-references: EMBL:U41746; PIDN:AAA83331.1; CESP:T18H9.2
C;Genetics:
A;Gene: CESP:T18H9.2
A;Introns: 4/3; 126/3; 161/3; 190/3; 239/3; 282/3; 401/1; 691/3

  Query Match             63.2%;  Score 91;  DB 2;  Length 709;
  Best Local Similarity   61.5%;  Pred. No. 1.3e-05;
  Matches   16;  Conservative    5;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 GYYVEMTVGSPPQTLNILVDTGSSNF 26
              ||  ::|||||||   :::|||||||
Db         39 GYVGKITVGSPPQEFRVIMDTGSSNF 64


RESULT 3
T47207
aspartic proteinase (EC 3.4.23.-) [imported] - Neurospora crassa
C;Species: Neurospora crassa
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: T47207
R;Bowman, B.
submitted to the EMBL Data Library, September 1995
A;Reference number: Z24391
A;Accession: T47207
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-396 <BOW>
A;Cross-references: UNIPROT:Q01294; EMBL:U36471; PIDN:AAA79878.1
C;Genetics:
A;Gene: pep-4
A;Introns: 33/3; 85/1
C;Superfamily: pepsin
C;Keywords: aspartic proteinase; hydrolase

  Query Match             62.5%;  Score 90;  DB 2;  Length 396;
  Best Local Similarity   55.6%;  Pred. No. 9.6e-06;
  Matches   15;  Conservative    7;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          2 YYVEMTVGSPPQTLNILVDTGSSNFAV 28
              |: |:|:|:|:|||  :::||||||  |
Db         85 YFSEITIGTPPQTFKVVLDTGSSNLWV 111


RESULT 4
A25379
saccharopepsin (EC 3.4.23.25) precursor - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein P2585; protein YPL154c; proteinase A; Saccharomyces aspartic
C;Species: Saccharomyces cerevisiae
C;Date: 25-Oct-1987 #sequence_revision 25-Oct-1987 #text_change 16-Aug-2004
C;Accession: A25379; A25378; A24711; B42640; S65165; S69445; S71635; S28231; S28233
R;Woolford, C.A.; Daniels, L.B.; Park, F.J.; Jones, E.W.; Van Arsdell, J.N.; Innis, M.A.
Mol. Cell. Biol. 6, 2500-2510, 1986
A;Title: The PEP4 gene encodes an aspartyl protease implicated in the posttranslational
A;Reference number: A25379; MUID:87064548; PMID:3537721
A;Accession: A25379
A;Molecule type: DNA
A;Residues: 1-405 <WOO>
A;Cross-references: UNIPROT:P07267; EMBL:M13358; NID:g172121; PIDN:AAB63975.1; PID:g1721
R;Ammerer, G.; Hunter, C.P.; Rothman, J.H.; Saari, G.C.; Valls, L.A.; Stevens, T.H.
Mol. Cell. Biol. 6, 2490-2499, 1986
A;Title: PEP4 gene of Saccharomyces cerevisiae encodes proteinase A, a vacuolar enzyme r
A;Reference number: A25378; MUID:87064547; PMID:3023936
A;Accession: A25378
A;Molecule type: DNA
A;Residues: 1-405 <AMM>
A;Cross-references: GB:M13358; GB:M13632; NID:g172121; PIDN:AAB63975.1; PID:g172122
R;Dreyer, T.; Halkier, B.; Svendsen, I.; Ottesen, M.
Carlsberg Res. Commun. 51, 27-41, 1986
A;Title: Primary structure of the aspartic proteinase A from Saccharomyces cerevisiae.
A;Reference number: A24711
A;Accession: A24711
A;Molecule type: protein
A;Residues: 77-405 <DRE>
R;Roof, D.M.; Meluh, P.B.; Rose, M.D.
J. Cell Biol. 118, 95-108, 1992
A;Title: Kinesin-related proteins required for assembly of the mitotic spindle.
A;Reference number: A42640; MUID:92317166; PMID:1618910
A;Accession: B42640
A;Molecule type: DNA
A;Residues: 373-405 <ROO>
A;Cross-references: EMBL:Z11963; NID:g3852; PIDN:CAA78020.1; PID:g3853
A;Note: the authors did not translate the codons for residues 373, 374, and 375
A;Note: sequence extracted from NCBI backbone (NCBIN:107719, NCBIP:107721)
R;Purnelle, B.; Coster, F.; Goffeau, A.
submitted to the Protein Sequence Database, May 1996
A;Reference number: S65154
A;Accession: S65165
A;Molecule type: DNA
A;Residues: 1-405 <PUR>
A;Cross-references: EMBL:Z73510; NID:g1370327; PIDN:CAA97859.1; PID:g1370328; MIPS:YPL15
A;Experimental source: strain S288C (AB972)
R;Purnelle, B.; Comblez, S.; Coster, F.; Naveau, F.; Goffeau, A.
submitted to the EMBL Data Library, March 1996
A;Description: The sequence of 55 kb on the left arm of yeast chromosome XVI identifies
ogue to the human phosphotyrosyl phosphatase activator PTPA and a homologue to the plant
A;Reference number: S69428
A;Accession: S69445
A;Molecule type: DNA
A;Residues: 1-405 <PUW>
A;Cross-references: EMBL:X96770; NID:g1403537; PIDN:CAA65567.1; PID:g1403555
R;Wolff, A.M.; Din, N.; Litske Petersen, J.G.
Yeast 12, 823-832, 1996
A;Title: Vacuolar and extracellular maturation of Saccharomyces cerevisiae proteinase A
A;Reference number: S71635; MUID:96437971; PMID:8840499
A;Accession: S71635
A;Molecule type: protein
A;Residues: 23-31;68-86 <WOL>
C;Genetics:
A;Gene: SGD:PEP4; PRA1; PHO9
A;Cross-references: SGD:S0006075; MIPS:YPL154c
A;Map position: 16L
C;Function:
A;Description: responsible for degradation of internalized alpha-factor receptor and a-f
 alkaline phosphatase, acid trehalase, and vacuolar exopolyphosphatase
C;Superfamily: Pepsin
C;Keywords: aspartic proteinase; hydrolase; yeast vacuole
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-67/Domain: propeptide #status experimental <PRO>
F;68-405/Product: saccharopepsin #status experimental <MAT>

  Query Match             60.4%;  Score 87;  DB 2;  Length 405;
  Best Local Similarity   51.9%;  Pred. No. 2.8e-05;
  Matches   14;  Conservative    7;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          2 YYVEMTVGSPPQTLNILVDTGSSNFAV 28
              || ::|:|:|||   :::||||||  |
Db         91 YYTDITLGTPPQNFKVILDTGSSNLWV 117


RESULT 5
T33383
hypothetical protein H22K11.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T33383
R;Beck, C.; Wamsley, P.; Keppler, N.
submitted to the EMBL Data Library, July 1998
A;Description: The sequence of C. elegans cosmid H22K11.
A;Reference number: Z21333
A;Accession: T33383
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-398 <BEC>
A;Cross-references: UNIPROT:P55956; EMBL:AF077544; PIDN:AAC64617.1; GSPDB:GN00028; CESP:I
A;Experimental source: strain Bristol N2; clone H22K11
```

```
C;Genetics:
A;Gene: CESP:H22K11.1
A;Map position: X
A;Introns: 20/2; 112/3; 147/3
C;Superfamily: pepsin

  Query Match             57.6%;  Score 83;  DB 2;  Length 398;
  Best Local Similarity   55.6%;  Pred. No. 0.00011;
  Matches   15;  Conservative    4;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          2 YYVEMTVGSPPQTLNILVDTGSSNFAV 28
              ||  :|:|:|||   :| ||||||  |
Db         69 YYGPVTIGTPPQNFQVLFDTGSSNLWV 95


RESULT 6
REHUK
renin (EC 3.4.23.15) precursor [validated] - human
N;Alternate names: angiotensinogenase
C;Species: Homo sapiens (man)
C;Date: 27-Nov-1985 #sequence_revision 30-Jun-1993 #text_change 16-Aug-2004
C;Accession: A21454; A21190; A21673; A00990; A26531; I52884; I55306; I53999; A35688; A36
R;Hardman, J.A.; Hort, Y.J.; Catanzaro, D.F.; Tellam, J.T.; Baxter, J.D.; Morris, B.J.;
DNA 3, 457-468, 1984
A;Title: Primary structure of the human renin gene.
A;Reference number: A21454; MUID:85076176; PMID:6391881
A;Accession: A21454
A;Molecule type: DNA
A;Residues: 1-406 <HAR>
A;Cross-references: UNIPROT:P00797; EMBL:X01732
R;Imai, T.; Miyazaki, H.; Hirose, S.; Hori, H.; Hayashi, T.; Kageyama, R.; Ohkubo, H.; N
Proc. Natl. Acad. Sci. U.S.A. 80, 7405-7409, 1983
A;Title: Cloning and sequence analysis of cDNA for human renin precursor.
A;Reference number: A21190; MUID:84170236; PMID:6324167
A;Accession: A21190
A;Molecule type: mRNA
A;Residues: 1-406 <IMA>
A;Cross-references: GB:L00073; EMBL:K01169; NID:g190992; PIDN:AAA60363.1; PID:g190994
R;Hobart, P.M.; Fogliano, M.; O'Connor, B.A.; Schaefer, I.M.; Chirgwin, J.M.
Proc. Natl. Acad. Sci. U.S.A. 81, 5026-5030, 1984
A;Title: Human renin gene: structure and sequence analysis.
A;Reference number: A21673; MUID:84298075; PMID:6089171
A;Accession: A21673
A;Molecule type: DNA
A;Residues: 1-230,234-403 <HOB>
A;Cross-references: EMBL:K02225
A;Experimental source: submandibular gland
R;Soubrier, F.; Panthier, J.J.; Corvol, P.; Rougeon, F.
Nucleic Acids Res. 11, 7181-7190, 1983
A;Title: Molecular cloning and nucleotide sequence of a human renin cDNA fragment.
A;Reference number: A00990; MUID:84041513; PMID:6138751
A;Accession: A00990
A;Molecule type: mRNA
A;Residues: 108-350,'I',352-406 <SOU>
A;Cross-references: EMBL:X00063
R;Fukamizu, A.; Nishi, K.; Nishimatsu, S.; Miyazaki, H.; Hirose, S.; Murakami, K.
Gene 49, 139-145, 1986
A;Title: Human renin gene of renin-secreting tumor.
A;Reference number: A26531; MUID:87191993; PMID:3032746
A;Accession: A26531
A;Molecule type: DNA
A;Residues: 1-33 <FUK>
A;Cross-references: GB:M15410; NID:g337341; PIDN:AAA60263.1; PID:g337342
A;Experimental source: JGC tumor genomic library
R;Morris, B.J.
Clin. Sci. 71, 345-355, 1986
A;Title: New possibilities for intracellular renin and inactive renin now that the struc
A;Reference number: I52884; MUID:87003365; PMID:3530608
A;Accession: I52884
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-54,'S',56-188,'Q',190-230,234-303,'C',305-406 <MOR>
A;Cross-references: GB:M26901; NID:g337345; PIDN:AAA60364.1; PID:g337347
R;Burt, D.W.; Nakamura, N.; Kelley, P.; Dzau, V.J.
J. Biol. Chem. 264, 7357-7362, 1989
A;Title: Identification of negative and positive regulatory elements in the human renin
A;Reference number: I55306; MUID:89214174; PMID:2540188
A;Accession: I55306
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-33 <BUR>
A;Cross-references: GB:M26440; NID:g341497; PIDN:AAA60365.1; PID:g620039
R;Soubrier, F.; Panthier, J.J.; Houot, A.M.; Rougeon, F.; Corvol, P.
Gene 41, 85-92, 1986
A;Title: Segmental homology between the promoter region of the human renin gene and the
A;Reference number: I53999; MUID:86193583; PMID:3516796
A;Accession: I53999
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-33 <SO2>
A;Cross-references: GB:M13253; NID:g190995; PIDN:AAA60262.1; PID:g190996
R;Vlahos, C.J.; Walls, J.D.; Berg, D.T.; Grinnell, B.W.
Biochem. Biophys. Res. Commun. 171, 375-383, 1990
A;Title: The purification and characterization of recombinant human renin expressed in
A;Reference number: A35688; MUID:90365733; PMID:2203348
A;Accession: A35688
A;Molecule type: protein
A;Residues: 67-84;120-137 <VLA>
R;Higashimori, K.; Mizuno, K.; Nakajo, S.; Boehm, F.H.; Marcotte, P.A.; Egan, D.A.; Hol
J. Biol. Chem. 264, 14662-14667, 1989
A;Title: Pure human inactive renin. Evidence that native inactive renin is prorenin.
A;Reference number: A36504; MUID:89359256; PMID:2670924
A;Accession: A36504
A;Molecule type: protein
A;Residues: 24-35 <HIG>
A;Experimental source: chorion laeve
R;Pratt, R.E.; Carleton, J.E.; Richie, J.P.; Heusser, C.; Dzau, V.J.
Proc. Natl. Acad. Sci. U.S.A. 84, 7837-7840, 1987
A;Title: Human renin biosynthesis and secretion in normal and ischemic kidneys.
A;Reference number: A39906; MUID:88068494; PMID:3317396
A;Contents: annotation; prorenin demonstrated by radiosequencing
R;Fritz, L.C.; Haidar, M.A.; Arfsten, A.E.; Schilling, J.W.; Carilli, C.; Shine, J.; Ba
J. Biol. Chem. 262, 12409-12412, 1987
A;Title: Human renin is correctly processed and targeted to the regulated secretory pat
A;Reference number: A27367; MUID:87308259; PMID:3305508
A;Contents: annotation; radiosequencing of propeptide and mature protein in recombinant
C;Comment: The only known function of renal renin is to release angiotensin I from angi
reased sodium retention by the kidney.
C;Comment: Renal renin is synthesized by the juxtaglomerular cells of the kidney in res
C;Genetics:
A;Gene: GDB:REN
A;Cross-references: GDB:120345; OMIM:179820
A;Map position: 1q32-1q32
A;Introns: 33/2; 83/3; 125/1; 164/3; 230/2; 233/2; 273/2; 320/3; 353/3
C;Superfamily: Pepsin
C;Keywords: aspartic proteinase; blood pressure control; glycoprotein; hydrolase; kidne
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-406/Product: prorenin #status experimental <PMAT>
F;24-66/Domain: propeptide #status experimental <PRO>
F;67-406/Product: renin #status experimental <MAT>
F;71/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;104,292/Active site: Asp #status predicted
F;117-124/Disulfide bonds: #status experimental
F;141/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;283-287,325-362/Disulfide bonds: #status predicted

  Query Match             57.6%;  Score 83;  DB 1;  Length 406;
  Best Local Similarity   58.3%;  Pred. No. 0.00012;
  Matches   14;  Conservative    5;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          2 YYVEMTVGSPPQTLNILVDTGSSN 25
              || |: :|:||||  :: ||||||
Db         86 YYGEIGIGTPPQTFKVVFDTGSSN 109


RESULT 7
```

```
JC7573
pepsinogen C - African clawed frog
N;Alternate names: progastricsin
C;Species: Xenopus laevis (African clawed frog)
C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
C;Accession: JC7573; PC7118
R;Ikuzawa, M.; Inokuchi, T.; Kobayashi, K.; Yasumasu, S.
J. Biochem. 129, 147-153, 2001
A;Title: Amphibian pepsinogens: Purification and characterization of Xenopus pepsinogens
A;Reference number: JC7573; MUID:21064922; PMID:11134969
A;Contents: Stomach
A;Accession: JC7573
A;Molecule type: mRNA
A;Residues: 1-383 <IKU>
A;Cross-references: UNIPROT:Q9DEC3; DDBJ:AB045379
A;Accession: PC7118
A;Molecule type: protein
A;Residues: 17-68 <IK2>
C;Comment: This protein is a zymogen for gastric aspartic proteinase, with pepsin-like a
C;Genetics:
A;Gene: PgC
C;Superfamily: pepsin
C;Keywords: stomach; zymogen

  Query Match             56.9%;  Score 82;  DB 2;  Length 383;
  Best Local Similarity   55.6%;  Pred. No. 0.00015;
  Matches   15;  Conservative    5;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          2 YYVEMTVGSPPQTLNILVDTGSSNFAV 28
              || |:::|:|||   :| ||||||  |
Db         67 YYGEISIGTPPQNFLVLFDTGSSNLWV 93


RESULT 8
A39314
gastricsin (EC 3.4.23.3) precursor - bullfrog
C;Species: Rana catesbeiana (bullfrog)
C;Date: 19-Jun-1992 #sequence_revision 19-Jun-1992 #text_change 16-Aug-2004
C;Accession: A39314
R;Yakabe, E.; Tanji, M.; Ichinose, M.; Goto, S.; Miki, K.; Kurokawa, K.; Ito, H.; Kageya
J. Biol. Chem. 266, 22436-22443, 1991
A;Title: Purification, characterization, and amino acid sequences of pepsinogens and pep
A;Reference number: A39314; MUID:92042186; PMID:1939266
A;Accession: A39314
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-384 <YAK>
A;Cross-references: UNIPROT:Q91322; GB:M73750; NID:g213687; PIDN:AAA49530.1; PID:g213688
C;Superfamily: Pepsin
C;Keywords: aspartic proteinase; hydrolase; protein digestion

  Query Match             56.9%;  Score 82;  DB 2;  Length 384;
  Best Local Similarity   55.6%;  Pred. No. 0.00015;
  Matches   15;  Conservative    5;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          2 YYVEMTVGSPPQTLNILVDTGSSNFAV 28
              || |:::|:|||   :| ||||||  |
Db         67 YYGEISIGTPPQNFLVLFDTGSSNLWV 93


RESULT 9
JE0371
pepsin C (EC 3.4.23.-) precursor - chicken
N;Alternate names: pepsinogen C
C;Species: Gallus gallus (chicken)
C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 09-Jul-2004
C;Accession: JE0371
R;Sakamoto, N.; Saiga, H.; Yasugi, S.
Biochem. Biophys. Res. Commun. 250, 420-424, 1998
A;Title: Analysis of temporal expression pattern and cis-regulatory sequences of chicken
A;Reference number: JE0370; MUID:98440813; PMID:9753645
A;Accession: JE0371
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-389 <SAK>
A;Cross-references: UNIPROT:Q9W643; UNIPROT:Q9PWK1
C;Superfamily: pepsin
C;Keywords: aspartic proteinase; hydrolase

  Query Match             56.9%;  Score 82;  DB 2;  Length 389;
  Best Local Similarity   55.6%;  Pred. No. 0.00016;
  Matches   15;  Conservative    5;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          2 YYVEMTVGSPPQTLNILVDTGSSNFAV 28
              || |:::|:|||   :| ||||||  |
Db         73 YYGEISIGTPPQNFLVLFDTGSSNLWV 99


RESULT 10
I47099
renin (EC 3.4.23.15) - sheep
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 15-Oct-1996 #sequence_revision 15-Oct-1996 #text_change 09-Jul-2004
C;Accession: I47099
R;Aldred, G.P.; Fu, P.; Crawford, R.J.; Fernley, R.T.
J. Mol. Endocrinol. 8, 3-11, 1992
A;Title: The sequence and tissue expression of ovine renin.
A;Reference number: I47099; MUID:92181567; PMID:1543532
A;Accession: I47099
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-400 <ALD>
A;Cross-references: UNIPROT:P52115; GB:L43524; NID:g896317; PIDN:AAA69809.1; PID:g89631
C;Superfamily: pepsin
C;Keywords: aspartic proteinase; hydrolase
F;98,286/Active site: Asp #status predicted

  Query Match             56.9%;  Score 82;  DB 2;  Length 400;
  Best Local Similarity   51.9%;  Pred. No. 0.00016;
  Matches   14;  Conservative    6;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          2 YYVEMTVGSPPQTLNILVDTGSSNFAV 28
              || |: :|:||||  :: ||||:|  |
Db         80 YYGEIGIGTPPQTFKVIFDTGSANLWV 106


RESULT 11
REMSS
renin (EC 3.4.23.15) precursor, submandibular - mouse
C;Species: Mus musculus (house mouse)
C;Date: 15-Oct-1982 #sequence_revision 17-Dec-1982 #text_change 16-Aug-2004
C;Accession: A93923; A93285; B93285; B22058; A00988
R;Misono, K.S.; Chang, J.J.; Inagami, T.
Proc. Natl. Acad. Sci. U.S.A. 79, 4858-4862, 1982
A;Title: Amino acid sequence of mouse submaxillary gland renin.
A;Reference number: A93923; MUID:83014991; PMID:6812055
A;Accession: A93923
A;Molecule type: protein
A;Residues: 64-351;354-401 <MIS>
A;Cross-references: UNIPROT:P00796
R;Panthier, J.J.; Foote, S.; Chambraud, B.; Strosberg, A.D.; Corvol, P.; Rougeon, F.
Nature 298, 90-92, 1982
A;Title: Complete amino acid sequence and maturation of the mouse submaxillary gland ren
A;Reference number: A93285; MUID:82220074; PMID:6283373
A;Accession: A93285
A;Molecule type: mRNA
A;Residues: 1-98,'M',100-194,'LSRS',199-394,'V',396-401 <PA1>
A;Cross-references: GB:J00621; GB:V00845; NID:g200701; PIDN:AAA40050.1; PID:g200702
A;Note: the authors translated codon ATG for residue 99 as Ile
A;Accession: B93285
A;Molecule type: protein
A;Residues: 64-84;354-374 <PA2>
R;Poe, M.; Liesch, J.M.
J. Biol. Chem. 258, 9856-9860, 1983
A;Title: Mouse submaxillary gland renin contains a noncovalently attached fatty acid.
A;Reference number: A92439; MUID:83290909; PMID:6350284
```

A;Contents: annotation; fatty acid binding
R;Panthier, J.J.; Dreyfus, M.; Roux, D.T.L.; Rougeon, F.
Proc. Natl. Acad. Sci. U.S.A. 81, 5489-5493, 1984
A;Title: Mouse kidney and submaxillary gland renin genes differ in their 5' putative reg
A;Reference number: A22058; MUID:84298161; PMID:6089205
A;Accession: B22058
A;Molecule type: DNA
A;Residues: 1-29 <PAN>
C;Comment: The enzyme contains a noncovalently attached fatty acid.
C;Comment: Submandibular renin has catalytic and antigenic activities similar to renal r
C;Comment: This renin is synthesized in the submandibular gland of males only.
C;Genetics:
A;Gene: REN2
C;Superfamily: Pepsin
C;Keywords: aspartic proteinase; hydrolase; salivary gland; submandibular gland
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-63/Domain: activation peptide #status predicted <ACP>
F;64-351/Product: renin, submandibular, heavy chain #status experimental <RSH>
F;354-401/Product: renin, submandibular, light chain #status experimental <RSL>
F;101,286/Active site: Asp #status experimental
F;114-121,277-281,320-357/Disulfide bonds: #status predicted

Query Match 56.9%; Score 82; DB 1; Length 401;
Best Local Similarity 51.9%; Pred. No. 0.00016;
Matches 14; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy 2 YYVEMTVGSPPQTLNILVDTGSSNFAV 28
|| |: :|:|||| :: ||||:| |
Db 83 YYGEIGIGTPPQTFKVIFDTGSANLWV 109

RESULT 12
REMSK
renin (EC 3.4.23.15) precursor, renal - mouse
N;Alternate names: angiotensin-forming enzyme; angiotensinogenase; renin 1
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 16-Aug-2004
C;Accession: A00989; S07636; A22766; A22058; I57576; A05137; JH0083
R;Holm, I.; Ollo, R.; Panthier, J.J.; Rougeon, F.
EMBO J. 3, 557-562, 1984
A;Title: Evolution of aspartyl proteases by gene duplication: the mouse renin gene is or
A;Reference number: A00989; MUID:84182525; PMID:6370686
A;Accession: A00989
A;Molecule type: DNA
A;Residues: 1-402 <HOL>
A;Cross-references: UNIPROT:P06281; EMBL:X00850
R;Kim, W.S.; Murakami, K.; Nakayama, K.
Nucleic Acids Res. 17, 9480, 1989
A;Title: Nucleotide sequence of a cDNA coding for mouse Ren1 preprorenin.
A;Reference number: S07636; MUID:90067953; PMID:2685761
A;Accession: S07636
A;Molecule type: mRNA
A;Residues: 1-402 <KIM>
A;Cross-references: EMBL:X16642; NID:g53930; PIDN:CAA34636.1; PID:g53931
R;Mullins, J.J.; Burt, D.W.; Windass, J.D.; McTurk, P.; George, H.; Brammar, W.J.
EMBO J. 1, 1461-1466, 1982
A;Title: Molecular cloning of two distinct renin genes from the DBA/2 mouse.
A;Reference number: A90968; MUID:84207899; PMID:6327270
A;Accession: A22766
A;Molecule type: mRNA
A;Residues: 269-314,'D',316 <MUL>
R;Panthier, J.J.; Dreyfus, M.; Roux, D.T.L.; Rougeon, F.
Proc. Natl. Acad. Sci. U.S.A. 81, 5489-5493, 1984
A;Title: Mouse kidney and submaxillary gland renin genes differ in their 5' putative reg
A;Reference number: A22058; MUID:84298161; PMID:6089205
A;Accession: A22058
A;Molecule type: DNA
A;Residues: 1-30 <PAN>
R;Field, L.J.; Philbrick, W.M.; Howles, P.N.; Dickinson, D.P.; McGowan, R.A.; Gross, K.W
Mol. Cell. Biol. 4, 2321-2331, 1984
A;Title: Expression of tissue-specific Ren-1 and Ren-2 genes of mice: Comparative analys
A;Reference number: I57576; MUID:85085936; PMID:6392850
A;Accession: I57576
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-31 <RES>
A;Cross-references: GB:K02800; NID:g200689; PIDN:AAA40044.1; PID:g200690
C;Comment: The only known function of renal renin is to release angiotensin I from angio
creased sodium retention by the kidney.
C;Comment: Renal renin is synthesized by the juxtaglomerular cells of the kidney in resp
C;Genetics:
A;Gene: Ren-1
A;Introns: 31/2; 81/3; 123/1; 162/3; 228/2; 268/2; 316/3; 349/3
C;Superfamily: Pepsin
C;Keywords: aspartic proteinase; blood pressure control; glycoprotein; hydrolase; kidney
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-64/Domain: propeptide #status predicted <PRO>
F;65-402/Product: renin #status predicted <MAT>
F;69,139,320/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;102,287/Active site: Asp #status predicted

Query Match 56.9%; Score 82; DB 1; Length 402;
Best Local Similarity 51.9%; Pred. No. 0.00016;
Matches 14; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy 2 YYVEMTVGSPPQTLNILVDTGSSNFAV 28
|| |: :|:|||| :: ||||:| |
Db 84 YYGEIGIGTPPQTFKVIFDTGSANLWV 110

RESULT 13
S71591
aspartic proteinase precursor, wound-induced - tomato
C;Species: Lycopersicon esculentum (tomato)
C;Date: 04-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
C;Accession: S71591
R;Schaller, A.; Ryan, C.A.
Plant Mol. Biol. 31, 1073-1077, 1996
A;Title: Molecular cloning of a tomato leaf cDNA encoding an aspartic protease, a system
A;Reference number: S71591; MUID:97000919; PMID:8843949
A;Accession: S71591
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-506 <SCH>
A;Cross-references: UNIPROT:Q40140; EMBL:L46681; NID:g951448; PIDN:AAB18280.1; PID:g9514
C;Superfamily: oryzasin; saposin repeat homology

Query Match 56.9%; Score 82; DB 2; Length 506;
Best Local Similarity 55.6%; Pred. No. 0.00021;
Matches 15; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Qy 2 YYVEMTVGSPPQTLNILVDTGSSNFAV 28
|| |: :||||| :: |||||| |
Db 83 YYGEIGIGSPPQKFKVIFDTGSSNLWV 109

RESULT 14
D85056
probable aspartic proteinase [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: D85056
R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sprin
Nature 402, 769-777, 1999
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A;Reference number: A85001; MUID:20083488; PMID:10617198
A;Accession: D85056
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-508 <STO>
A;Cross-references: UNIPROT:Q9XEC4; GB:NC_001268; NID:g7267203; PIDN:CAB77914.1; GSPDB:C
C;Genetics:
A;Gene: AT4g04460
A;Map position: 4
C;Superfamily: oryzasin; saposin repeat homology

```
  Query Match             56.9%;  Score 82;  DB 2;  Length 508;
  Best Local Similarity   54.2%;  Pred. No. 0.00021;
  Matches   13;  Conservative    6;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          2 YYVEMTVGSPPQTLNILVDTGSSN 25
              || ::|:|:|||   :: ||||||
Db         87 YYGDITIGTPPQKFTVIFDTGSSN 110


RESULT 15
S49349
cyprosin (EC 3.4.23.-) - cardoon
C;Species: Cynara cardunculus (cardoon)
C;Date: 16-Feb-1995 #sequence_revision 12-May-1995 #text_change 09-Jul-2004
C;Accession: S49349
R;Pietrzak, M.; Brodelius, P.; Pais, M.S.
submitted to the EMBL Data Library, September 1994
A;Reference number: S49349
A;Accession: S49349
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-509 <PIE>
A;Cross-references: UNIPROT:Q39476; EMBL:X81984; NID:g556818; PIDN:CAA57510.1; PID:g5568
C;Comment: The pair of saposin repeat homology domains tagged SAP1 and SAP2 represent a
C;Superfamily: oryzasin; saposin repeat homology
C;Keywords: aspartic proteinase; hydrolase
F;316-361/Domain: saposin repeat homology #status atypical <SAP1>
F;375-420/Domain: saposin repeat homology #status atypical <SAP2>
F;103,290/Active site: Asp #status predicted

  Query Match             56.9%;  Score 82;  DB 2;  Length 509;
  Best Local Similarity   55.6%;  Pred. No. 0.00021;
  Matches   15;  Conservative    4;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          2 YYVEMTVGSPPQTLNILVDTGSSNFAV 28
              || |: :|||||   :: ||||||  |
Db         85 YYGEIGIGSPPQKFTVIFDTGSSNLWV 111


Search completed: July 26, 2005, 16:47:58
Job time : 40 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: July 26, 2005, 16:37:25 ; Search time 167 Seconds
(without alignments)
85.858 Million cell updates/sec

Title: US-10-726-967A-52
Perfect score: 144
Sequence: 1 GYYVEMTVGSPPQTLNILVDTGSSNFAV 28

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	144	100.0	127	2	Q76KP0	Q76kp0 homo sapien
2	144	100.0	467	2	Q8C4F4	Q8c4f4 mus musculu
3	144	100.0	501	1	BAE1_HUMAN	P56817 homo sapien
4	144	100.0	501	1	BAE1_MOUSE	P56818 mus musculu
5	144	100.0	501	1	BAE1_RAT	P56819 r beta-secr
6	144	100.0	501	2	Q8IYC8	Q8iyc8 homo sapien
7	144	100.0	501	2	Q8BQY4	Q8bqy4 mus musculu
8	144	100.0	532	2	Q9ULS1	Q9uls1 homo sapien
9	143	99.3	501	2	Q8C7R1	Q8c7r1 mus musculu
10	124	86.1	505	2	Q6NZT7	Q6nzt7 brachydanio
11	122	84.7	500	2	Q7T0Y2	Q7t0y2 xenopus lae
12	120	83.3	499	2	Q6PB20	Q6pb20 xenopus lae
13	119	82.6	396	2	Q9NZL1	Q9nzl1 homo sapien
14	119	82.6	439	2	Q9H2V8	Q9h2v8 homo sapien
15	119	82.6	468	2	Q9NZL2	Q9nzl2 homo sapien
16	119	82.6	518	1	BAE2_HUMAN	Q9y5z0 homo sapien
17	116	80.6	514	2	Q6IE75	Q6ie75 rattus norv
18	116	80.6	514	2	Q8C5E9	Q8c5e9 mus musculu
19	116	80.6	514	2	Q8C793	Q8c793 mus musculu
20	116	80.6	514	2	Q9JL18	Q9jl18 mus musculu
21	100	69.4	244	2	Q8WQY9	Q8wqy9 aphrocallis
22	93	64.6	423	2	Q8N2D4	Q8n2d4 homo sapien
23	91	63.2	396	2	Q6C080	Q6c080 yarrowia li
24	90	62.5	396	1	CARP_NEUCR	Q01294 neurospora
25	90	62.5	396	2	Q7RVB0	Q7rvb0 neurospora
26	90	62.5	409	2	Q6CRW3	Q6crw3 kluyveromyc
27	89	61.8	173	2	Q96TV7	Q96tv7 pleurotus o
28	89	61.8	427	2	P91802	P91802 schistosoma
29	89	61.8	428	2	Q7JNB4	Q7jnb4 schistosoma
30	89	61.8	429	2	Q26515	Q26515 schistosoma
31	87	60.4	405	1	CARP_YEAST	P07267 saccharomyc
32	86	59.7	398	2	Q6H2K5	Q6h2k5 botrytis ci
33	86	59.7	400	2	Q86ZP8	Q86zp8 paracoccidi
34	86	59.7	504	2	Q93XR0	Q93xr0 ipomoea bat
35	85	59.0	354	2	Q9GYX7	Q9gyx7 boophilus m
36	84	58.3	397	2	Q8NJS2	Q8njs2 leptosphaer
37	84	58.3	401	2	Q6INM6	Q6inm6 xenopus lae
38	84	58.3	406	2	Q6DLW5	Q6dlw5 macaca mula
39	83	57.6	358	2	Q9FRW5	Q9frw5 nepenthes a
40	83	57.6	398	1	ASP3_CAEEL	P55956 caenorhabdi
41	83	57.6	400	1	RENI_CALJA	Q9tsz1 callithrix
42	83	57.6	403	2	Q6T5C2	Q6t5c2 homo sapien
43	83	57.6	406	1	RENI_HUMAN	P00797 homo sapien
44	83	57.6	406	1	RENI_PANTR	P60016 pan troglod
45	83	57.6	406	2	Q6DLS0	Q6dls0 macaca fasc

ALIGNMENTS

RESULT 1
Q76KP0
ID Q76KP0 PRELIMINARY; PRT; 127 AA.
AC Q76KP0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Beta-site APP cleaving enzyme isoform I-127.
GN Name=BACE;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tanahashi H.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
CC -!- SIMILARITY: Belongs to peptidase family A1.
DR EMBL; AB089958; BAC81826.1; -.
DR HSSP; P00797; 1BBS.
DR GO; GO:0009049; F:aspartic-type signal peptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001461; Peptidase_A1.
DR InterPro; IPR009119; Pept_A1_BACE.
DR InterPro; IPR009120; Pept_A1_BACE1.
DR InterPro; IPR009007; Pept_Aspartic.
DR InterPro; IPR001969; Pept_Asp_AS.
DR Pfam; PF00026; Asp; 1.
DR PRINTS; PR01816; BACE1.
DR PRINTS; PR01815; BACEFAMILY.
DR PROSITE; PS00141; ASP_PROTEASE; 1.
KW Aspartyl protease; Hydrolase; Protease.
SQ SEQUENCE 127 AA; 13939 MW; C657354CBEE72DC4 CRC64;

Query Match 100.0%; Score 144; DB 2; Length 127;
Best Local Similarity 100.0%; Pred. No. 4.6e-14;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GYYVEMTVGSPPQTLNILVDTGSSNFAV 28
              ||||||||||||||||||||||||||||
Db         74 GYYVEMTVGSPPQTLNILVDTGSSNFAV 101
```

RESULT 2
Q8C4F4
ID Q8C4F4 PRELIMINARY; PRT; 467 AA.
AC Q8C4F4;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus 0 day neonate cerebellum cDNA, RIKEN full-length enriched
DE library, clone:C230037E16 product:beta-site APP cleaving enzyme, full
DE insert sequence.
GN Name=Bace1; Synonyms=Bace;

```
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Meth. Enzymol. 303:19-44(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   RIKEN FANTOM Consortium;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Cerebellum;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [6]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Cerebellum;
RA   Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA   Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA   Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA   Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA   Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA   Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA   Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA   Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA   Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA   Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA   Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to peptidase family A1.
DR   EMBL; AK082317; BAC38462.1; -.
DR   HSSP; P56817; 1FKN.
DR   MGD; MGI:1346542; Bace1.
DR   GO; GO:0005768; C:endosome; ISS.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   GO; GO:0005794; C:Golgi apparatus; ISS.
DR   GO; GO:0016021; C:integral to membrane; ISS.
DR   GO; GO:0004190; F:aspartic-type endopeptidase activity; ISS.
DR   GO; GO:0050435; P:beta-amyloid metabolism; ISS.
DR   GO; GO:0006509; P:membrane protein ectodomain proteolysis; ISS.
DR   InterPro; IPR001461; Peptidase_A1.
DR   InterPro; IPR009119; Pept_A1_BACE.
DR   InterPro; IPR009120; Pept_A1_BACE1.
DR   InterPro; IPR009007; Pept_Aspartic.
DR   InterPro; IPR001969; Pept_Asp_AS.
DR   PRINTS; PR01816; BACE1.
DR   PRINTS; PR01815; BACEFAMILY.
DR   PRINTS; PR00792; PEPSIN.
DR   PROSITE; PS00141; ASP_PROTEASE; 1.
KW   Aspartyl protease; Hydrolase; Protease.
SQ   SEQUENCE   467 AA;  52063 MW;  31AB674FF1843652 CRC64;

  Query Match           100.0%;  Score 144;  DB 2;  Length 467;
  Best Local Similarity  100.0%;  Pred. No. 2.2e-13;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GYYVEMTVGSPPQTLNILVDTGSSNFAV 28
              ||||||||||||||||||||||||||||
Db         74 GYYVEMTVGSPPQTLNILVDTGSSNFAV 101


RESULT 3
BAE1_HUMAN
ID   BAE1_HUMAN     STANDARD;      PRT;   501 AA.
AC   P56817; Q9BYB9; Q9BYC0; Q9BYC1; Q9UJT5;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Beta-secretase 1 precursor (EC 3.4.23.46) (Beta-site APP cleaving
DE   enzyme 1) (Beta-site amyloid precursor protein cleaving enzyme 1)
DE   (Aspartyl protease 2) (Asp 2) (ASP2) (Membrane-associated aspartic
DE   protease 2) (Memapsin-2).
GN   Name=BACE1; Synonyms=BACE;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM A).
RC   TISSUE=Brain;
RX   MEDLINE=20002972; PubMed=10531052; DOI=10.1126/science.286.5440.735;
RA   Vassar R., Bennett B.D., Babu-Khan S., Kahn S., Mendiaz E.A.,
RA   Denis P., Teplow D.B., Ross S., Amarante P., Loeloff R., Luo Y.,
RA   Fisher S., Fuller J., Edenson S., Lile J., Jarosinski M.A.,
RA   Biere A.L., Curran E., Burgess T., Louis J.-C., Collins F.,
RA   Treanor J., Rogers G., Citron M.;
RT   "Beta-secretase cleavage of Alzheimer's amyloid precursor protein by
RT   the transmembrane aspartic protease BACE.";
RL   Science 286:735-741(1999).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM A), SEQUENCE OF 46-68, AND
RP   CHARACTERIZATION.
RC   TISSUE=Brain;
RX   MEDLINE=20057171; PubMed=10591214; DOI=10.1038/990114;
RA   Sinha S., Anderson J.P., Barbour R., Basi G.S., Caccavello R.,
RA   Davis D., Doan M., Dovey H.F., Frigon N., Hong J., Jacobson-Croak K.,
RA   Jewett N., Keim P., Knops J., Lieberburg I., Power M., Tan H.,
RA   Tatsuno G., Tung J., Schenk D., Seubert P., Suomensaari S.M., Wang S.,
RA   Walker D., Zhao J., McConlogue L., Varghese J.;
RT   "Purification and cloning of amyloid precursor protein beta-secretase
RT   from human brain.";
RL   Nature 402:537-540(1999).
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORM A).
RX   MEDLINE=20057170; PubMed=10591213; DOI=10.1038/990107;
RA   Yan R., Bienkowski M.J., Shuck M.E., Miao H., Tory M.C., Pauley A.M.,
RA   Brashier J.R., Stratman N.C., Mathews W.R., Buhl A.E., Carter D.B.,
RA   Tomasselli A.G., Parodi L.A., Heinrikson R.L., Gurney M.E.;
RT   "Membrane-anchored aspartyl protease with Alzheimer's disease beta-
RT   secretase activity.";
RL   Nature 402:533-537(1999).
```

```
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORM A).
RX   MEDLINE=20120043; PubMed=10656250; DOI=10.1006/mcne.1999.0811;
RA   Hussain I., Powell D.J., Howlett D.R., Tew D.G., Meek T.D.,
RA   Chapman C., Gloger I.S., Murphy K.E., Southan C.D., Ryan D.M.,
RA   Smith T.S., Simmons D.L., Walsh F.S., Dingwall C., Christie G.;
RT   "Identification of a novel aspartic proteinase (Asp 2) as beta-
RT   secretase.";
RL   Mol. Cell. Neurosci. 14:419-427(1999).
RN   [5]
RP   SEQUENCE FROM N.A. (ISOFORM B).
RC   TISSUE=Brain, and Pancreas;
RA   Michel B., De Pietri Tonelli D., Zacchetti D., Keller P.;
RT   "New beta-site APP cleaving enzyme isoform (BACE-1B) obtained from
RT   human brain and pancreas.";
RL   Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   SEQUENCE FROM N.A. (ISOFORM C).
RC   TISSUE=Pancreas;
RA   Zacchetti D., De Pietri Tonelli D., Schnurbus R.;
RT   "New beta-site APP cleaving enzyme isoform (BACE-1C) obtained from
RT   human pancreas.";
RL   Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
RN   [7]
RP   SEQUENCE FROM N.A. (ISOFORMS B; C AND D).
RC   TISSUE=Brain;
RX   MEDLINE=21408467; PubMed=11516562; DOI=10.1016/S0304-3940(01)01912-7;
RA   Tanahashi H., Tabira T.;
RT   "Three novel alternatively spliced isoforms of the human beta-site
RT   amyloid precursor protein cleaving enzyme (BACE) and their effect on
RT   amyloid beta-peptide production.";
RL   Neurosci. Lett. 307:9-12(2001).
RN   [8]
RP   SEQUENCE OF 14-501 FROM N.A. (ISOFORM A), AND CHARACTERIZATION.
RX   MEDLINE=20144060; PubMed=10677483; DOI=10.1073/pnas.97.4.1456;
RA   Lin X., Koelsch G., Wu S., Downs D., Dashti A., Tang J.;
RT   "Human aspartic protease memapsin 2 cleaves the beta-secretase site of
RT   beta-amyloid precursor protein.";
RL   Proc. Natl. Acad. Sci. U.S.A. 97:1456-1460(2000).
RN   [9]
RP   DISULFIDE BONDS.
RX   MEDLINE=21950860; PubMed=11953458;
RA   Fischer F., Molinari M., Bodendorf U., Paganetti P.;
RT   "The disulphide bonds in the catalytic domain of BACE are critical but
RT   not essential for amyloid precursor protein processing activity.";
RL   J. Neurochem. 80:1079-1088(2002).
CC   -!- FUNCTION: Responsible for the proteolytic processing of the
CC       amyloid precursor protein (APP). Cleaves at the amino terminus of
CC       the A-beta peptide sequence, between residues 671 and 672 of APP,
CC       leads to the generation and extracellular release of beta-cleaved
CC       soluble APP, and a corresponding cell-associated carboxy-terminal
CC       fragment which is later released by gamma-secretase.
CC   -!- CATALYTIC ACTIVITY: Broad endopeptidase specificity. Cleaves Glu-
CC       Val-Asn-Leu-|-Asp-Ala-Glu-Phe in the Swedish variant of
CC       Alzheimer's amyloid precursor protein.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=4;
CC       Name=A; Synonyms=BACE-1A, BAC-501;
CC         IsoId=P56817-1; Sequence=Displayed;
CC       Name=B; Synonyms=BACE-1B, BACE-I-476;
CC         IsoId=P56817-2; Sequence=VSP_005223;
CC       Name=C; Synonyms=BACE-1C, BACE-I-457;
CC         IsoId=P56817-3; Sequence=VSP_005222;
CC       Name=D; Synonyms=BACE-1D, BACE-I-432;
CC         IsoId=P56817-4; Sequence=VSP_005222, VSP_005223;
CC   -!- TISSUE SPECIFICITY: Brain.
CC   -!- SIMILARITY: Belongs to the peptidase A1 family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF190725; AAF04142.1; -.
DR   EMBL; AF201468; AAF18982.1; -.
DR   EMBL; AF200343; AAF17079.1; -.
DR   EMBL; AF204943; AAF26367.1; -.
DR   EMBL; AF338816; AAK38374.1; -.
DR   EMBL; AF338817; AAK38375.1; -.
DR   EMBL; AB050436; BAB40931.1; -.
DR   EMBL; AB050437; BAB40932.1; -.
DR   EMBL; AB050438; BAB40933.1; -.
DR   EMBL; AF200193; AAF13715.1; -.
DR   PIR; A59090; A59090.
DR   PDB; 1FKN; X-ray; A/B=56-446.
DR   PDB; 1M4H; X-ray; A/B=56-446.
DR   MEROPS; A01.004; -.
DR   Genew; HGNC:933; BACE1.
DR   H-InvDB; HIX0010165; -.
DR   MIM; 604252; -.
DR   GO; GO:0005887; C:integral to plasma membrane; TAS.
DR   GO; GO:0008798; F:beta-aspartyl-peptidase activity; TAS.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; TAS.
DR   InterPro; IPR009119; Pept_A1_BACE.
DR   InterPro; IPR009120; Pept_A1_BACE1.
DR   InterPro; IPR001969; Pept_Asp_AS.
DR   InterPro; IPR009007; Pept_Aspartic.
DR   InterPro; IPR001461; Peptidase_A1.
DR   Pfam; PF00026; Asp; 1.
DR   PRINTS; PR01816; BACE1.
DR   PRINTS; PR01815; BACEFAMILY.
DR   PRINTS; PR00792; PEPSIN.
DR   PROSITE; PS00141; ASP_PROTEASE; 1.
KW   3D-structure; Alternative splicing; Aspartyl protease;
KW   Direct protein sequencing; Glycoprotein; Hydrolase; Signal;
KW   Transmembrane; Zymogen.
FT   SIGNAL       1     21       Potential.
FT   PROPEP      22     45
FT   CHAIN       46    501       Beta-secretase 1.
FT   DOMAIN      22    457       Extracellular (Potential).
FT   TRANSMEM   458    478       Potential.
FT   DOMAIN     479    501       Cytoplasmic (Potential).
FT   ACT_SITE    93     93       By similarity.
FT   ACT_SITE   289    289       By similarity.
FT   DISULFID   216    420
FT   DISULFID   278    443
FT   DISULFID   330    380
FT   CARBOHYD   153    153       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   172    172       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   223    223       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   354    354       N-linked (GlcNAc. . .) (Potential).
FT   VARSPLIC   146    189       Missing (in isoform C and isoform D).
FT                               /FTId=VSP_005222.
FT   VARSPLIC   190    214       Missing (in isoform B and isoform D).
FT                               /FTId=VSP_005223.
FT   HELIX       61     63
FT   TURN        64     65
FT   STRAND      67     70
FT   TURN        71     73
FT   STRAND      74     81
FT   TURN        82     85
FT   STRAND      86     93
FT   TURN        94     95
FT   STRAND      99    102
FT   TURN       107    108
FT   HELIX      115    117
FT   TURN       119    120
FT   STRAND     122    131
FT   STRAND     136    147
FT   TURN       149    150
FT   STRAND     155    167
FT   TURN       172    173
```

```
FT   STRAND       178    181
FT   HELIX        185    187
FT   TURN         192    193
FT   HELIX        197    204
FT   STRAND       211    215
FT   HELIX        224    229

  Query Match             100.0%;  Score 144;  DB 1;  Length 501;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-13;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GYYVEMTVGSPPQTLNILVDTGSSNFAV 28
              ||||||||||||||||||||||||||||
Db         74 GYYVEMTVGSPPQTLNILVDTGSSNFAV 101


RESULT 4
BAE1_MOUSE
ID   BAE1_MOUSE     STANDARD;      PRT;   501 AA.
AC   P56818;
DT   30-MAY-2000 (Rel. 39, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Beta-secretase 1 precursor (EC 3.4.23.46) (Beta-site APP cleaving
DE   enzyme 1) (Beta-site amyloid precursor protein cleaving enzyme 1)
DE   (Aspartyl protease 2) (Asp 2) (ASP2) (Membrane-associated aspartic
DE   protease 2) (Memapsin-2).
GN   Name=Bace1; Synonyms=Bace;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20002972; PubMed=10531052; DOI=10.1126/science.286.5440.735;
RA   Vassar R., Bennett B.D., Babu-Khan S., Kahn S., Mendiaz E.A.,
RA   Denis P., Teplow D.B., Ross S., Amarante P., Loeloff R., Luo Y.,
RA   Fisher S., Fuller J., Edenson S., Lile J., Jarosinski M.A.,
RA   Biere A.L., Curran E., Burgess T., Louis J.-C., Collins F.,
RA   Treanor J., Rogers G., Citron M.;
RT   "Beta-secretase cleavage of Alzheimer's amyloid precursor protein by
RT   the transmembrane aspartic protease BACE.";
RL   Science 286:735-741(1999).
RN   [2]
RP   REVISIONS TO 6 AND 81-87.
RA   Bennett B.D., Vassar R., Citron M.;
RL   Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20057170; PubMed=10591213; DOI=10.1038/990107;
RA   Yan R., Bienkowski M.J., Shuck M.E., Miao H., Tory M.C., Pauley A.M.,
RA   Brashier J.R., Stratman N.C., Mathews W.R., Buhl A.E., Carter D.B.,
RA   Tomasselli A.G., Parodi L.A., Heinrikson R.L., Gurney M.E.;
RT   "Membrane-anchored aspartyl protease with Alzheimer's disease beta-
RT   secretase activity.";
RL   Nature 402:533-537(1999).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Head;
RX   MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA   Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA   Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA   Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA   Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA   Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA   Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA   Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA   Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA   Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA   Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA   Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA   Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA   Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA   Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA   Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA   Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA   Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA   Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA   Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA   Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA   Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA   Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA   Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA   Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA   Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA   Birney E., Hayashizaki Y.;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6; TISSUE=Brain;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- FUNCTION: Responsible for the proteolytic processing of the
CC       amyloid precursor protein (APP). Cleaves at the amino terminus of
CC       the A-beta peptide sequence, between residues 671 and 672 of APP,
CC       leads to the generation and extracellular release of beta-cleaved
CC       soluble APP, and a corresponding cell-associated carboxy-terminal
CC       fragment which is later released by gamma-secretase (By
CC       similarity).
CC   -!- CATALYTIC ACTIVITY: Broad endopeptidase specificity. Cleaves Glu-
CC       Val-Asn-Leu-|-Asp-Ala-Glu-Phe in the Swedish variant of
CC       Alzheimer's amyloid precursor protein.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- TISSUE SPECIFICITY: Brain.
CC   -!- SIMILARITY: Belongs to the peptidase A1 family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF190726; AAF04143.2; -.
DR   EMBL; AF200346; AAF17082.1; -.
DR   EMBL; AK014464; BAB29370.1; -.
DR   EMBL; BC048189; AAH48189.1; -.
DR   HSSP; P56817; 1M4H.
DR   MEROPS; A01.004; -.
DR   MGD; MGI:1346542; Bace1.
DR   InterPro; IPR009119; Pept_A1_BACE.
DR   InterPro; IPR009120; Pept_A1_BACE1.
DR   InterPro; IPR001969; Pept_Asp_AS.
DR   InterPro; IPR009007; Pept_Aspartic.
```

```
DR   InterPro; IPR001461; Peptidase_A1.
DR   Pfam; PF00026; Asp; 1.
DR   PRINTS; PR01816; BACE1.
DR   PRINTS; PR01815; BACEFAMILY.
DR   PRINTS; PR00792; PEPSIN.
DR   PROSITE; PS00141; ASP_PROTEASE; 1.
KW   Aspartyl protease; Glycoprotein; Hydrolase; Signal; Transmembrane;
KW   Zymogen.
FT   SIGNAL       1     21       Potential.
FT   PROPEP      22     45       Potential.
FT   CHAIN       46    501       Beta-secretase 1.
FT   DOMAIN      22    457       Extracellular (Potential).
FT   TRANSMEM   458    478       Potential.
FT   DOMAIN     479    501       Cytoplasmic (Potential).
FT   ACT_SITE    93     93       By similarity.
FT   ACT_SITE   289    289       By similarity.
FT   DISULFID   216    420       By similarity.
FT   DISULFID   278    443       By similarity.
FT   DISULFID   330    380       By similarity.
FT   CARBOHYD   153    153       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   172    172       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   223    223       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   354    354       N-linked (GlcNAc. . .) (Potential).
SQ   SEQUENCE   501 AA;  55747 MW;  C085A013145E474E CRC64;

  Query Match             100.0%;  Score 144;  DB 1;  Length 501;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-13;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GYYVEMTVGSPPQTLNILVDTGSSNFAV 28
              ||||||||||||||||||||||||||||
Db         74 GYYVEMTVGSPPQTLNILVDTGSSNFAV 101


RESULT 5
BAE1_RAT
ID   BAE1_RAT       STANDARD;      PRT;   501 AA.
AC   P56819;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Beta-secretase 1 precursor (EC 3.4.23.46) (Beta-site APP cleaving
DE   enzyme 1) (Beta-site amyloid precursor protein cleaving enzyme 1)
DE   (Aspartyl protease 2) (Asp 2) (ASP2) (Membrane-associated aspartic
DE   protease 2) (Memapsin-2).
GN   Name=Bace1; Synonyms=Bace;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20002972; PubMed=10531052; DOI=10.1126/science.286.5440.735;
RA   Vassar R., Bennett B.D., Babu-Khan S., Kahn S., Mendiaz E.A.,
RA   Denis P., Teplow D.B., Ross S., Amarante P., Loeloff R., Luo Y.,
RA   Fisher S., Fuller J., Edenson S., Lile J., Jarosinski M.A.,
RA   Biere A.L., Curran E., Burgess T., Louis J.-C., Collins F.,
RA   Treanor J., Rogers G., Citron M.;
RT   "Beta-secretase cleavage of Alzheimer's amyloid precursor protein by
RT   the transmembrane aspartic protease BACE.";
RL   Science 286:735-741(1999).
CC   -!- FUNCTION: Responsible for the proteolytic processing of the
CC       amyloid precursor protein (APP). Cleaves at the amino terminus of
CC       the A-beta peptide sequence, between residues 671 and 672 of APP,
CC       leads to the generation and extracellular release of beta-cleaved
CC       soluble APP, and a corresponding cell-associated carboxy-terminal
CC       fragment which is later released by gamma-secretase (By
CC       similarity).
CC   -!- CATALYTIC ACTIVITY: Broad endopeptidase specificity. Cleaves Glu-
CC       Val-Asn-Leu-|-Asp-Ala-Glu-Phe in the Swedish variant of
CC       Alzheimer's amyloid precursor protein.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: Belongs to the peptidase A1 family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF190727; AAF04144.1; -.
DR   HSSP; P56817; 1M4H.
DR   MEROPS; A01.004; -.
DR   RGD; 2191; Bace.
DR   InterPro; IPR009119; Pept_A1_BACE.
DR   InterPro; IPR009120; Pept_A1_BACE1.
DR   InterPro; IPR001969; Pept_Asp_AS.
DR   InterPro; IPR009007; Pept_Aspartic.
DR   InterPro; IPR001461; Peptidase_A1.
DR   Pfam; PF00026; Asp; 1.
DR   PRINTS; PR01816; BACE1.
DR   PRINTS; PR01815; BACEFAMILY.
DR   PRINTS; PR00792; PEPSIN.
DR   PROSITE; PS00141; ASP_PROTEASE; 1.
KW   Aspartyl protease; Glycoprotein; Hydrolase; Signal; Transmembrane;
KW   Zymogen.
FT   SIGNAL       1     21       Potential.
FT   PROPEP      22     45       Potential.
FT   CHAIN       46    501       Beta-secretase 1.
FT   DOMAIN      22    457       Extracellular (Potential).
FT   TRANSMEM   458    478       Potential.
FT   DOMAIN     479    501       Cytoplasmic (Potential).
FT   ACT_SITE    93     93       By similarity.
FT   ACT_SITE   289    289       By similarity.
FT   DISULFID   216    420       By similarity.
FT   DISULFID   278    443       By similarity.
FT   DISULFID   330    380       By similarity.
FT   CARBOHYD   153    153       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   172    172       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   223    223       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   354    354       N-linked (GlcNAc. . .) (Potential).
SQ   SEQUENCE   501 AA;  55806 MW;  24B445BC8BE87DE3 CRC64;

  Query Match             100.0%;  Score 144;  DB 1;  Length 501;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-13;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GYYVEMTVGSPPQTLNILVDTGSSNFAV 28
              ||||||||||||||||||||||||||||
Db         74 GYYVEMTVGSPPQTLNILVDTGSSNFAV 101


RESULT 6
Q8IYC8
ID   Q8IYC8       PRELIMINARY;      PRT;   501 AA.
AC   Q8IYC8;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Beta-site APP-cleaving enzyme 1, isoform A preproprotein.
GN   Name=BACE1;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
```

```
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Strausberg R.;
RL   Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to peptidase family A1.
DR   EMBL; BC036084; AAH36084.1; -.
DR   HSSP; P56817; 1FKN.
DR   GO; GO:0005768; C:endosome; ISS.
DR   GO; GO:0005794; C:Golgi apparatus; ISS.
DR   GO; GO:0016021; C:integral to membrane; ISS.
DR   GO; GO:0004190; F:aspartic-type endopeptidase activity; ISS.
DR   GO; GO:0050435; P:beta-amyloid metabolism; ISS.
DR   GO; GO:0006509; P:membrane protein ectodomain proteolysis; ISS.
DR   InterPro; IPR001461; Peptidase_A1.
DR   InterPro; IPR009119; Pept_A1_BACE.
DR   InterPro; IPR009120; Pept_A1_BACE1.
DR   InterPro; IPR009007; Pept_Aspartic.
DR   InterPro; IPR001969; Pept_Asp_AS.
DR   PRINTS; PR01816; BACE1.
DR   PRINTS; PR01815; BACEFAMILY.
DR   PRINTS; PR00792; PEPSIN.
DR   PROSITE; PS00141; ASP_PROTEASE; 1.
KW   Aspartyl protease; Hydrolase; Protease.
SQ   SEQUENCE   501 AA;  55823 MW;  768595CF5517EFB7 CRC64;

  Query Match             100.0%;  Score 144;  DB 2;  Length 501;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-13;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GYYVEMTVGSPPQTLNILVDTGSSNFAV 28
              ||||||||||||||||||||||||||||
Db         74 GYYVEMTVGSPPQTLNILVDTGSSNFAV 101


RESULT 7
Q8BQY4
ID   Q8BQY4       PRELIMINARY;      PRT;   501 AA.
AC   Q8BQY4;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Mus musculus adult male corpora quadrigemina cDNA, RIKEN full-length
DE   enriched library, clone:B230346M13 product:beta-site APP cleaving
DE   enzyme, full insert sequence.
GN   Name=Bace1; Synonyms=Bace;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Meth. Enzymol. 303:19-44(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   RIKEN FANTOM Consortium;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [6]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
RA   Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA   Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA   Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA   Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA   Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA   Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA   Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA   Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA   Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA   Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA   Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to peptidase family A1.
DR   EMBL; AK046175; BAC32620.1; -.
DR   HSSP; P56817; 1FKN.
DR   MGD; MGI:1346542; Bace1.
DR   GO; GO:0005768; C:endosome; ISS.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   GO; GO:0005794; C:Golgi apparatus; ISS.
DR   GO; GO:0016021; C:integral to membrane; ISS.
DR   GO; GO:0004190; F:aspartic-type endopeptidase activity; ISS.
DR   GO; GO:0050435; P:beta-amyloid metabolism; ISS.
DR   GO; GO:0006509; P:membrane protein ectodomain proteolysis; ISS.
DR   InterPro; IPR001461; Peptidase_A1.
DR   InterPro; IPR009119; Pept_A1_BACE.
DR   InterPro; IPR009120; Pept_A1_BACE1.
DR   InterPro; IPR009007; Pept_Aspartic.
DR   InterPro; IPR001969; Pept_Asp_AS.
DR   PRINTS; PR01816; BACE1.
DR   PRINTS; PR01815; BACEFAMILY.
DR   PRINTS; PR00792; PEPSIN.
DR   PROSITE; PS00141; ASP_PROTEASE; 1.
KW   Aspartyl protease; Hydrolase; Protease.
```

```
SQ   SEQUENCE   501 AA;  55816 MW;  C0855513145E024E CRC64;

  Query Match             100.0%;  Score 144;  DB 2;  Length 501;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-13;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GYYVEMTVGSPPQTLNILVDTGSSNFAV 28
              ||||||||||||||||||||||||||||
Db         74 GYYVEMTVGSPPQTLNILVDTGSSNFAV 101


RESULT 8
Q9ULS1
ID   Q9ULS1      PRELIMINARY;      PRT;   532 AA.
AC   Q9ULS1;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   KIAA1149 protein (Fragment).
GN   Name=KIAA1149;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=20039618; PubMed=10574461;
RA   Hirosawa M., Nagase T., Ishikawa K., Kikuno R., Nomura N., Ohara O.;
RT   "Characterization of cDNA clones selected by the GeneMark analysis
RT   from size-fractionated cDNA libraries from human brain.";
RL   DNA Res. 6:329-336(1999).
CC   -!- SIMILARITY: Belongs to peptidase family A1.
DR   EMBL; AB032975; BAA86463.2; -.
DR   HSSP; P56817; 1FKN.
DR   GO; GO:0005768; C:endosome; ISS.
DR   GO; GO:0005794; C:Golgi apparatus; ISS.
DR   GO; GO:0016021; C:integral to membrane; ISS.
DR   GO; GO:0004190; F:aspartic-type endopeptidase activity; ISS.
DR   GO; GO:0050435; P:beta-amyloid metabolism; ISS.
DR   GO; GO:0006509; P:membrane protein ectodomain proteolysis; ISS.
DR   InterPro; IPR001461; Peptidase_A1.
DR   InterPro; IPR009119; Pept_A1_BACE.
DR   InterPro; IPR009120; Pept_A1_BACE1.
DR   InterPro; IPR009007; Pept_Aspartic.
DR   InterPro; IPR001969; Pept_Asp_AS.
DR   PRINTS; PR01816; BACE1.
DR   PRINTS; PR01815; BACEFAMILY.
DR   PRINTS; PR00792; PEPSIN.
DR   PROSITE; PS00141; ASP_PROTEASE; 1.
KW   Aspartyl protease; Hydrolase; Protease.
FT   NON_TER       1       1
SQ   SEQUENCE   532 AA;  58720 MW;  98B135D0D5FBD2E8 CRC64;

  Query Match             100.0%;  Score 144;  DB 2;  Length 532;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-13;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GYYVEMTVGSPPQTLNILVDTGSSNFAV 28
              ||||||||||||||||||||||||||||
Db        105 GYYVEMTVGSPPQTLNILVDTGSSNFAV 132


RESULT 9
Q8C7R1
ID   Q8C7R1      PRELIMINARY;      PRT;   501 AA.
AC   Q8C7R1;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Mus musculus 12 days embryo spinal cord cDNA, RIKEN full-length
DE   enriched library, clone:C530008K17 product:beta-site APP cleaving
DE   enzyme, full insert sequence.
GN   Name=Bace1; Synonyms=Bace;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Spinal cord;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Meth. Enzymol. 303:19-44(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Spinal cord;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   RIKEN FANTOM Consortium;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Spinal cord;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Spinal cord;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Spinal cord;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [6]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Spinal cord;
RA   Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA   Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA   Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA   Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA   Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA   Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA   Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA   Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA   Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA   Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA   Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to peptidase family A1.
DR   EMBL; AK049626; BAC33844.1; -.
DR   HSSP; P56817; 1FKN.
DR   MGD; MGI:1346542; Bace1.
DR   GO; GO:0005768; C:endosome; ISS.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   GO; GO:0005794; C:Golgi apparatus; ISS.
DR   GO; GO:0016021; C:integral to membrane; ISS.
```

```
DR   GO; GO:0004190; F:aspartic-type endopeptidase activity; ISS.
DR   GO; GO:0050435; P:beta-amyloid metabolism; ISS.
DR   GO; GO:0006509; P:membrane protein ectodomain proteolysis; ISS.
DR   InterPro; IPR001461; Peptidase_A1.
DR   InterPro; IPR009119; Pept_A1_BACE.
DR   InterPro; IPR009120; Pept_A1_BACE1.
DR   InterPro; IPR009007; Pept_Aspartic.
DR   InterPro; IPR001969; Pept_Asp_AS.
DR   PRINTS; PR01816; BACE1.
DR   PRINTS; PR01815; BACEFAMILY.
DR   PRINTS; PR00792; PEPSIN.
DR   PROSITE; PS00141; ASP_PROTEASE; 1.
KW   Aspartyl protease; Hydrolase; Protease.
SQ   SEQUENCE   501 AA;  55761 MW;  B410DA8B64647663 CRC64;

  Query Match             99.3%;  Score 143;  DB 2;  Length 501;
  Best Local Similarity   96.4%;  Pred. No. 3.4e-13;
  Matches   27;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GYYVEMTVGSPPQTLNILVDTGSSNFAV 28
              |||||||:||||||||||||||||||||
Db         74 GYYVEMTIGSPPQTLNILVDTGSSNFAV 101


RESULT 10
Q6NZT7
ID   Q6NZT7      PRELIMINARY;      PRT;   505 AA.
AC   Q6NZT7;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein zgc:77409.
GN   Name=zgc:77409;
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RA   Director MGC Project;
RL   Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to peptidase family A1.
DR   EMBL; BC065973; AAH65973.1; -.
DR   HSSP; P56272; 1AM5.
DR   ZFIN; ZDB-GENE-040426-1835; zgc:77409.
DR   GO; GO:0009049; F:aspartic-type signal peptidase activity; IEA.
DR   GO; GO:0004194; F:pepsin A activity; IEA.
DR   GO; GO:0008233; F:peptidase activity; IEA.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR   InterPro; IPR001461; Peptidase_A1.
DR   InterPro; IPR009119; Pept_A1_BACE.
DR   InterPro; IPR009120; Pept_A1_BACE1.
DR   InterPro; IPR009007; Pept_Aspartic.
DR   InterPro; IPR001969; Pept_Asp_AS.
DR   PRINTS; PR01816; BACE1.
DR   PRINTS; PR01815; BACEFAMILY.
DR   PRINTS; PR00792; PEPSIN.
DR   PROSITE; PS00141; ASP_PROTEASE; 1.
KW   Aspartyl protease; Hydrolase; Hypothetical protein; Protease.
SQ   SEQUENCE   505 AA;  55661 MW;  6C83DA4CFD903BAD CRC64;

  Query Match             86.1%;  Score 124;  DB 2;  Length 505;
  Best Local Similarity   85.7%;  Pred. No. 3e-10;
  Matches   24;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GYYVEMTVGSPPQTLNILVDTGSSNFAV 28
              |||:|| |||| | ||||||||||||||
Db         79 GYYIEMAVGSPAQRLNILVDTGSSNFAV 106


RESULT 11
Q7T0Y2
ID   Q7T0Y2      PRELIMINARY;      PRT;   500 AA.
AC   Q7T0Y2;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Bace2-prov protein.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RX   MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA   Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA   Richardson P.;
RT   "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT   initiative.";
RL   Dev. Dyn. 225:384-391(2002).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RA   Klein S., Strausberg R.;
```

```
RL   Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC055989; AAH55989.1; -.
DR   HSSP; P56817; 1FKN.
DR   GO; GO:0004194; F:pepsin A activity; IEA.
DR   GO; GO:0008233; F:peptidase activity; IEA.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR   InterPro; IPR009007; Pept_Aspartic.
DR   InterPro; IPR001969; Pept_Asp_AS.
DR   PROSITE; PS00141; ASP_PROTEASE; 2.
SQ   SEQUENCE   500 AA;  54722 MW;  10F16756CAFDCD0B CRC64;

  Query Match             84.7%;  Score 122;  DB 2;  Length 500;
  Best Local Similarity   78.6%;  Pred. No. 6e-10;
  Matches   22;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GYYVEMTVGSPPQTLNILVDTGSSNFAV 28
              |||:|: :||||| :||||||||||||||
Db         75 GYYLELLIGSPPQKVNILVDTGSSNFAV 102


RESULT 12
Q6PB20
ID   Q6PB20      PRELIMINARY;      PRT;   499 AA.
AC   Q6PB20;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   MGC68482 protein.
GN   Name=MGC68482;
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RX   MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA   Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA   Richardson P.;
RT   "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT   initiative.";
RL   Dev. Dyn. 225:384-391(2002).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RA   Klein S., Strausberg R.;
RL   Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to peptidase family A1.
DR   EMBL; BC059963; AAH59963.1; -.
DR   HSSP; P20142; 1AVF.
DR   GO; GO:0009049; F:aspartic-type signal peptidase activity; IEA.
DR   GO; GO:0004194; F:pepsin A activity; IEA.
DR   GO; GO:0008233; F:peptidase activity; IEA.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR   InterPro; IPR001461; Peptidase_A1.
DR   InterPro; IPR009119; Pept_A1_BACE.
DR   InterPro; IPR009121; Pept_A1_BACE2.
DR   InterPro; IPR009007; Pept_Aspartic.
DR   InterPro; IPR001969; Pept_Asp_AS.
DR   PRINTS; PR01817; BACE2.
DR   PRINTS; PR01815; BACEFAMILY.
DR   PRINTS; PR00792; PEPSIN.
DR   PROSITE; PS00141; ASP_PROTEASE; 2.
KW   Aspartyl protease; Hydrolase; Protease.
SQ   SEQUENCE   499 AA;  54803 MW;  E846674A5DF6F8AF CRC64;

  Query Match             83.3%;  Score 120;  DB 2;  Length 499;
  Best Local Similarity   75.0%;  Pred. No. 1.2e-09;
  Matches   21;  Conservative    5;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GYYVEMTVGSPPQTLNILVDTGSSNFAV 28
              ||:|:|: :|:||| :||||||||||||
Db         74 GYYMELLIGTPPQKMNILVDTGSSNFAV 101


RESULT 13
Q9NZL1
ID   Q9NZL1      PRELIMINARY;      PRT;   396 AA.
AC   Q9NZL1;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Aspartyl protease.
GN   Name=BACE2;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20422477; PubMed=10965118;
RA   Solans A., Estivill X., de La Luna S.;
RT   "A new aspartyl protease on 21q22.3, BACE2, is highly similar to
RT   Alzheimer's amyloid precursor protein beta-secretase.";
RL   Cytogenet. Cell Genet. 89:177-184(2000).
CC   -!- SIMILARITY: Belongs to peptidase family A1.
DR   EMBL; AF188277; AAF35836.1; -.
DR   HSSP; P56817; 1FKN.
DR   GO; GO:0016021; C:integral to membrane; ISS.
DR   GO; GO:0006509; P:membrane protein ectodomain proteolysis; ISS.
DR   GO; GO:0042985; P:negative regulation of amyloid precursor pr. . .; ISS.
DR   GO; GO:0016486; P:peptide hormone processing; ISS.
DR   InterPro; IPR001461; Peptidase_A1.
DR   InterPro; IPR009119; Pept_A1_BACE.
DR   InterPro; IPR009121; Pept_A1_BACE2.
DR   InterPro; IPR009007; Pept_Aspartic.
DR   InterPro; IPR001969; Pept_Asp_AS.
DR   PRINTS; PR01817; BACE2.
DR   PRINTS; PR01815; BACEFAMILY.
DR   PRINTS; PR00792; PEPSIN.
DR   PROSITE; PS00141; ASP_PROTEASE; 2.
KW   Aspartyl protease; Hydrolase; Protease.
SQ   SEQUENCE   396 AA;  43013 MW;  5023A7AF391CEAC9 CRC64;

  Query Match             82.6%;  Score 119;  DB 2;  Length 396;
  Best Local Similarity   78.6%;  Pred. No. 1.3e-09;
  Matches   22;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GYYVEMTVGSPPQTLNILVDTGSSNFAV 28
              |||:|| :|:||| | ||||||||||||
Db         91 GYYLEMLIGTPPQKLQILVDTGSSNFAV 118
```

```
RESULT 14
Q9H2V8
ID   Q9H2V8      PRELIMINARY;      PRT;   439 AA.
AC   Q9H2V8;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   CDA13.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Pheochromocytoma;
RA   Li Y., Huang Q., Peng, y, Song H., Yu Y., Xu S., Ren S., Chen Z.,
RA   Han Z.;
RL   Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to peptidase family A1.
DR   EMBL; AF212252; AAG41783.1; -.
DR   HSSP; P56817; 1FKN.
DR   GO; GO:0016021; C:integral to membrane; ISS.
DR   GO; GO:0006509; P:membrane protein ectodomain proteolysis; ISS.
DR   GO; GO:0042985; P:negative regulation of amyloid precursor pr. . .; ISS.
DR   GO; GO:0016486; P:peptide hormone processing; ISS.
DR   InterPro; IPR001461; Peptidase_A1.
DR   InterPro; IPR009119; Pept_A1_BACE.
DR   InterPro; IPR009121; Pept_A1_BACE2.
DR   InterPro; IPR009007; Pept_Aspartic.
DR   InterPro; IPR001969; Pept_Asp_AS.
DR   PRINTS; PR01817; BACE2.
DR   PRINTS; PR01815; BACEFAMILY.
DR   PRINTS; PR00792; PEPSIN.
DR   PROSITE; PS00141; ASP_PROTEASE; 2.
KW   Aspartyl protease; Hydrolase; Protease.
SQ   SEQUENCE   439 AA;  48275 MW;  02EC0E0E50F11602 CRC64;

  Query Match             82.6%;  Score 119;  DB 2;  Length 439;
  Best Local Similarity   78.6%;  Pred. No. 1.5e-09;
  Matches   22;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GYYVEMTVGSPPQTLNILVDTGSSNFAV 28
              |||:|| :|:||| | ||||||||||||
Db         12 GYYLEMLIGTPPQKLQILVDTGSSNFAV 39


RESULT 15
Q9NZL2
ID   Q9NZL2      PRELIMINARY;      PRT;   468 AA.
AC   Q9NZL2;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Aspartyl protease.
GN   Name=BACE2;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20422477; PubMed=10965118;
RA   Solans A., Estivill X., de La Luna S.;
RT   "A new aspartyl protease on 21q22.3, BACE2, is highly similar to
RT   Alzheimer's amyloid precursor protein beta-secretase.";
RL   Cytogenet. Cell Genet. 89:177-184(2000).
CC   -!- SIMILARITY: Belongs to peptidase family A1.
DR   EMBL; AF188276; AAF35835.1; -.
DR   HSSP; P56817; 1FKN.
DR   GO; GO:0016021; C:integral to membrane; ISS.
DR   GO; GO:0006509; P:membrane protein ectodomain proteolysis; ISS.
DR   GO; GO:0042985; P:negative regulation of amyloid precursor pr. . .; ISS.
DR   GO; GO:0016486; P:peptide hormone processing; ISS.
DR   InterPro; IPR001461; Peptidase_A1.
DR   InterPro; IPR009119; Pept_A1_BACE.
DR   InterPro; IPR009121; Pept_A1_BACE2.
DR   InterPro; IPR009007; Pept_Aspartic.
DR   InterPro; IPR001969; Pept_Asp_AS.
DR   PRINTS; PR01817; BACE2.
DR   PRINTS; PR01815; BACEFAMILY.
DR   PRINTS; PR00792; PEPSIN.
DR   PROSITE; PS00141; ASP_PROTEASE; 2.
KW   Aspartyl protease; Hydrolase; Protease.
SQ   SEQUENCE   468 AA;  50324 MW;  717E0920126A0142 CRC64;

  Query Match             82.6%;  Score 119;  DB 2;  Length 468;
  Best Local Similarity   78.6%;  Pred. No. 1.6e-09;
  Matches   22;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GYYVEMTVGSPPQTLNILVDTGSSNFAV 28
              |||:|| :|:||| | ||||||||||||
Db         91 GYYLEMLIGTPPQKLQILVDTGSSNFAV 118


Search completed: July 26, 2005, 16:47:14
Job time : 169 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: July 26, 2005, 16:34:25 ; Search time 165 Seconds
(without alignments)
65.632 Million cell updates/sec

Title: US-10-726-967A-52
Perfect score: 144
Sequence: 1 GYYVEMTVGSPPQTLNILVDTGSSNFAV 28

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	144	100.0	28	8	ADP83926	Adp83926 Human BAC
2	144	100.0	387	4	AAU23068	Aau23068 Novel hum
3	144	100.0	390	4	AAU23069	Aau23069 Novel hum
4	144	100.0	391	7	ADC81581	Adc81581 Beta-secr
5	144	100.0	403	8	ADI64643	Adi64643 Mature hu
6	144	100.0	408	8	ADI64644	Adi64644 Mature hu
7	144	100.0	411	8	ADI64640	Adi64640 Mature hu
8	144	100.0	411	8	ADJ57790	Adj57790 BACE WT R
9	144	100.0	411	8	ADJ57791	Adj57791 BACE N-Q
10	144	100.0	414	6	ABR61930	Abr61930 Human pro
11	144	100.0	414	7	ADC72735	Adc72735 Human bet
12	144	100.0	415	3	AAB07899	Aab07899 Amino aci
13	144	100.0	417	8	ADJ57792	Adj57792 BACE N-Q
14	144	100.0	425	3	AAY88437	Aay88437 Human Asp
15	144	100.0	425	4	AAU07214	Aau07214 T7-caspas
16	144	100.0	425	4	AAE10641	Aae10641 T7-Caspas
17	144	100.0	425	4	AAE06871	Aae06871 T7-Caspas
18	144	100.0	425	4	AAE02593	Aae02593 T7-Caspas
19	144	100.0	425	4	AAU06615	Aau06615 T7-Caspas
20	144	100.0	425	5	ABB78602	Abb78602 T7-caspas
21	144	100.0	425	7	ADC81580	Adc81580 Beta-secr
22	144	100.0	425	8	ADJ94340	Adj94340 Human T7-
23	144	100.0	425	8	ADO50436	Ado50436 T7-Caspas
24	144	100.0	425	8	ADR75349	Adr75349 T7-Caspas
25	144	100.0	428	4	AAU07219	Aau07219 Human asp
26	144	100.0	428	4	AAE10646	Aae10646 Human-Asp
27	144	100.0	428	4	AAE06891	Aae06891 Human-Asp
28	144	100.0	428	4	AAE02598	Aae02598 Human asp
29	144	100.0	428	4	AAU06620	Aau06620 Human-pro
30	144	100.0	428	5	ABB78607	Abb78607 Human Asp
31	144	100.0	428	8	ADJ94363	Adj94363 Human-pro
32	144	100.0	428	8	ADO50459	Ado50459 Human Asp
33	144	100.0	428	8	ADR75372	Adr75372 Human Asp
34	144	100.0	432	7	ADC81561	Adc81561 Mature BA
35	144	100.0	433	3	AAY88433	Aay88433 Human-pro
36	144	100.0	433	4	AAU07213	Aau07213 T7-human
37	144	100.0	433	4	AAE10640	Aae10640 Human-pro
38	144	100.0	433	4	AAE06870	Aae06870 Human-pro
39	144	100.0	433	4	AAE02592	Aae02592 Human-pro
40	144	100.0	433	4	AAU06614	Aau06614 Human-pro
41	144	100.0	433	5	ABB78601	Abb78601 Human-pro
42	144	100.0	433	8	ADJ94338	Adj94338 Human-pro
43	144	100.0	433	8	ADO50434	Ado50434 Human-pro
44	144	100.0	433	8	ADP83954	Adp83954 Human BAC
45	144	100.0	433	8	ADP83951	Adp83951 Human BAC

ALIGNMENTS

RESULT 1
ADP83926
ID ADP83926 standard; peptide; 28 AA.
XX
AC ADP83926;
XX
DT 23-SEP-2004 (first entry)
XX
DE Human BACE1 isoform A protease domain SEQ ID NO:52.
XX
KW human; beta-site amyloid precursor protein cleaving enzyme 1;
KW beta-site APP cleaving enzyme 1; BACE1; BACE1 isoform A; prodomain;
KW engineered cleavage site; protease domain; neuroprotective; nootropic;
KW gene therapy; Alzheimer's disease; Down's syndrome.
XX
OS Homo sapiens.
XX
PN WO2004056962-A2.
XX
PD 08-JUL-2004.
XX
PF 02-DEC-2003; 2003WO-US038314.
XX
PR 04-DEC-2002; 2002US-0430984P.
XX
PA (SUNE-) SUNESIS PHARM INC.
XX
PI Ballinger M;
XX
DR WPI; 2004-507703/48.
XX
PT New polypeptides for producing homogenously processed preparations of
PT beta site amyloid precursor protein-cleaving enzyme comprises a
PT prodomain, an engineered cleavage site and a protease domain.
XX
PS Claim 5; SEQ ID NO 52; 40pp; English.
XX
CC The present invention describes a polypeptide (I) comprising in order
CC from the N-terminus to the C-terminus: (a) a prodomain comprising at
CC least 6 contiguous amino acids of the 16 amino acid sequence of SEQ ID
CC NO:3 (ADP83877, comprising residues 22-37 of SEQ ID NO:1 (ADP83876) which
CC is the longest isoform of human beta-site amyloid precursor protein (APP)
CC cleaving enzyme 1 (BACE1), isoform A); (b) an engineered cleavage site;
CC and (c) a protease domain. (I) is capable of being cleaved at the
CC engineered cleavage site, and so releases a free protease domain that has
CC BACE1 activity. Also described: (1) a nucleic acid sequence encoding (I);
CC (2) a vector for expression of (I); and (3) a host cell expressing (I).
CC (I) has neuroprotective and nootropic activities, and can be used in gene

CC therapy. (I) can be used for producing preparations of homogenously
CC processed BACE that may be used for e.g. studying or treating diseases
CC such as Alzheimer's disease or Down's syndrome. The human BACE1 gene is
CC located on chromosome 11, more specifically to 11q23.2-23.3. The present
CC sequence represents a human BACE1 isoform A protease domain amino acid
CC sequence, which is used in the exemplification of the present invention.
XX
SQ Sequence 28 AA;

Query Match 100.0%; Score 144; DB 8; Length 28;
Best Local Similarity 100.0%; Pred. No. 6.9e-15;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GYYVEMTVGSPPQTLNILVDTGSSNFAV 28
              ||||||||||||||||||||||||||||
Db          1 GYYVEMTVGSPPQTLNILVDTGSSNFAV 28
```

RESULT 2
AAU23068
ID AAU23068 standard; protein; 387 AA.
XX
AC AAU23068;
XX
DT 17-DEC-2001 (first entry)
XX
DE Novel human enzyme polypeptide #154.
XX
KW Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase;
KW ligase; hyperproliferative disorder; immunodeficiency disorder;
KW autoimmune disorder; neurological disorder; metabolic disorder;
KW inflammatory disorder; cardiovascular disorder; reproductive disorder;
KW blood-related disorder; infectious disorder; cytostatic; anti arthritic;
KW nephrotropic; anticoagulant.
XX
OS Homo sapiens.
XX
PN WO200155301-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US001239.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226868P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.

PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-465566/50.
DR N-PSDB; AAS40938.
XX
PT Novel polypeptides and polynucleotides useful for diagnosing, preventing,
PT treating neural, immune system, muscular, reproductive, pulmonary,
PT cardiovascular, renal, proliferative disorders and cancerous diseases.
XX
PS Claim 11; SEQ ID NO 1064; 1180pp; English.
XX
CC The present invention relates to the isolation of novel human enzyme
CC polypeptides, and the cDNA (AAS40785-AAS41684) and genomic sequences
CC encoding them. The enzyme polypeptides of the invention may comprise the
CC functional classes of oxidoreductases, transferases, hydrolases, lyases,
CC isomerases or ligases. The sequences of the invention are useful in the
CC diagnosis, treatment, prevention and/or prognosis of a wide range of
CC disorders including hyperproliferative disorders (e.g. cancer),
CC immunodeficiency disorders (e.g. AIDS) autoimmune disorders (e.g.
CC arthritis), neurological disorders (e.g. Alzheimer's disease), metabolic
CC disorders (e.g. phenylketonuria), inflammatory disorders (e.g. asthma),
CC cardiovascular disorders (e.g. atherosclerosis), blood-related disorders
CC (e.g. haemophilia), reproductive disorders (e.g. infertility) and
CC infectious disorders (e.g. Influenza). The polynucleotides of the
CC invention can also be used in gene therapy. AAU22915-AAU23814 represent
CC the novel human enzyme polypeptides of the invention. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 387 AA;

Query Match 100.0%; Score 144; DB 4; Length 387;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYYVEMTVGSPPQTLNILVDTGSSNFAV 28
||||||||||||||||||||||||||||
Db 10 GYYVEMTVGSPPQTLNILVDTGSSNFAV 37

RESULT 3
AAU23069
ID AAU23069 standard; protein; 390 AA.
XX
AC AAU23069;
XX
DT 17-DEC-2001 (first entry)
XX
DE Novel human enzyme polypeptide #155.
XX
KW Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase;
KW ligase; hyperproliferative disorder; immunodeficiency disorder;
KW autoimmune disorder; neurological disorder; metabolic disorder;
KW inflammatory disorder; cardiovascular disorder; reproductive disorder;
KW blood-related disorder; infectious disorder; cytostatic; anti arthritic;
KW nephrotropic; anticoagulant.
XX
OS Homo sapiens.
XX
PN WO200155301-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US001239.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226868P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.

PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-465566/50.
DR N-PSDB; AAS40939.
XX
PT Novel polypeptides and polynucleotides useful for diagnosing, preventing,
PT treating neural, immune system, muscular, reproductive, pulmonary,
PT cardiovascular, renal, proliferative disorders and cancerous diseases.
XX
PS Claim 11; SEQ ID NO 1065; 1180pp; English.
XX
CC The present invention relates to the isolation of novel human enzyme
CC polypeptides, and the cDNA (AAS40785-AAS41684) and genomic sequences
CC encoding them. The enzyme polypeptides of the invention may comprise the
CC functional classes of oxidoreductases, transferases, hydrolases, lyases,
CC isomerases or ligases. The sequences of the invention are useful in the
CC diagnosis, treatment, prevention and/or prognosis of a wide range of
CC disorders including hyperproliferative disorders (e.g. cancer),
CC immunodeficiency disorders (e.g. AIDS) autoimmune disorders (e.g.
CC arthritis), neurological disorders (e.g. Alzheimer's disease), metabolic
CC disorders (e.g. phenylketonuria), inflammatory disorders (e.g. asthma),
CC cardiovascular disorders (e.g. atherosclerosis), blood-related disorders
CC (e.g. haemophilia), reproductive disorders (e.g. infertility) and
CC infectious disorders (e.g. Influenza). The polynucleotides of the
CC invention can also be used in gene therapy. AAU22915-AAU23814 represent
CC the novel human enzyme polypeptides of the invention. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 390 AA;

Query Match 100.0%; Score 144; DB 4; Length 390;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYYVEMTVGSPPQTLNILVDTGSSNFAV 28
||||||||||||||||||||||||||||
Db 13 GYYVEMTVGSPPQTLNILVDTGSSNFAV 40

RESULT 4
ADC81581
ID ADC81581 standard; protein; 391 AA.
XX
AC ADC81581;
XX
DT 01-JAN-2004 (first entry)
XX
DE Beta-secretase (1fkn) amino acid sequence SEQ ID NO:4.
XX

KW human; BACE; modification; Pro33Lys; pro-enzyme.
XX
OS Unidentified.
XX
PN WO2003072733-A2.
XX
PD 04-SEP-2003.
XX
PF 21-FEB-2003; 2003WO-US005508.
XX
PR 21-FEB-2002; 2002US-0358651P.
XX
PA (PHAA) PHARMACIA & UPJOHN CO.
XX
PI Chou K, Howe JW;
XX
DR WPI; 2003-712719/67.
XX
PT BACE polypeptides having Pro33Lys modification, useful in determining
PT possible mutations, which will inhibit enzyme activity, and in
PT determining potential active site for target molecules.
XX
PS Disclosure; Fig 3; 38pp; English.
XX
CC The present invention describes an isolated polypeptide (I) comprising or
CC consisting of a fully defined sequence of 432 amino acids (see ADC81561),
CC and comprising human BACE having the modification Pro33Lys. Also
CC described: (1) a composition comprising an active human BACE enzyme
CC comprising the pro-enzyme sequence of BACE having the modification
CC Pro33Lys; (2) an isolated polynucleotide comprising a sequence encoding
CC (I); (3) an isolated polynucleotide consisting or comprising of
CC nucleotides 70-1365 of a 1355-bp sequence (see ADC81562); (4) an
CC expression vector comprising the polynucleotide of (2), or a
CC polynucleotide sequence encoding a Pro33Lys-BACE polypeptide, where the
CC expression vector can produce the Pro33Lys-BACE polypeptide when present
CC in a compatible host cell, when cultured under conditions that allow
CC production; (5) a recombinant host cell comprising the expression vector;
CC and (6) producing a (active) Pro33Lys-BACE polypeptide. The BACE
CC polypeptide having Pro33Lys modification may be used in determining
CC possible mutations, which will inhibit enzyme activity, and in
CC determining potential active site for target molecules. The vector
CC comprising the BACE polynucleotide is useful for producing recombinant
CC BACE polypeptides having Pro33Lys modification. The present sequence
CC represents a beta-secretase amino acid sequence, which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 391 AA;

Query Match 100.0%; Score 144; DB 7; Length 391;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYYVEMTVGSPPQTLNILVDTGSSNFAV 28
||||||||||||||||||||||||||||
Db 19 GYYVEMTVGSPPQTLNILVDTGSSNFAV 46

RESULT 5
ADI64643
ID ADI64643 standard; protein; 403 AA.
XX
AC ADI64643;
XX
DT 22-APR-2004 (first entry)
XX
DE Mature human beta-secretase (BACE) protein seq id 4.
XX
KW crystal; glycosylated human beta-secretase; BACE; human beta-secretase;
KW protein co-ordinate data.
XX
OS Homo sapiens.
XX
PN US2004014194-A1.
XX
PD 22-JAN-2004.
XX
PF 26-MAR-2003; 2003US-00400273.
XX
PR 27-MAR-2002; 2002US-0367937P.
XX
PA (SCHE) SCHERING CORP.
XX
PI Beyer BM, Hammond GS, Reichert P, Strickland C, Wang W, Weber PC;
PI Wong GT, Zhang L;
XX
DR WPI; 2004-167920/16.
XX
PT New crystal comprising a glycosylated, human beta-secretase polypeptide,
PT useful for determining the three-dimensional structure of beta-secretase
PT and other related proteins.
XX
PS Claim 5; SEQ ID NO 4; 107pp; English.
XX
CC The invention describes a crystal comprising a glycosylated, human beta-
CC secretase polypeptide characterised by structural coordinates comprising
CC a root mean square deviation of conserved residue backbone atoms of less
CC than 1.5 Angstrom when superimposed on backbone atoms described by
CC structural coordinates. The crystal is useful for determining the three-
CC dimensional structure of beta-secretase and other related proteins. This
CC is the amino acid sequence of a mature human beta-secretase (BACE)
CC protein.
XX
SQ Sequence 403 AA;

Query Match 100.0%; Score 144; DB 8; Length 403;
Best Local Similarity 100.0%; Pred. No. 1.7e-13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYYVEMTVGSPPQTLNILVDTGSSNFAV 28
||||||||||||||||||||||||||||
Db 27 GYYVEMTVGSPPQTLNILVDTGSSNFAV 54

RESULT 6
ADI64644
ID ADI64644 standard; protein; 408 AA.
XX
AC ADI64644;
XX
DT 22-APR-2004 (first entry)
XX
DE Mature human beta-secretase (BACE) protein seq id 5.
XX
KW crystal; glycosylated human beta-secretase; BACE; human beta-secretase;
KW protein co-ordinate data.
XX
OS Homo sapiens.
XX
PN US2004014194-A1.
XX
PD 22-JAN-2004.
XX
PF 26-MAR-2003; 2003US-00400273.
XX
PR 27-MAR-2002; 2002US-0367937P.
XX
PA (SCHE) SCHERING CORP.
XX
PI Beyer BM, Hammond GS, Reichert P, Strickland C, Wang W, Weber PC;
PI Wong GT, Zhang L;
XX
DR WPI; 2004-167920/16.
XX
PT New crystal comprising a glycosylated, human beta-secretase polypeptide,
PT useful for determining the three-dimensional structure of beta-secretase
PT and other related proteins.

XX
PS Claim 5; SEQ ID NO 5; 107pp; English.
XX
CC The invention describes a crystal comprising a glycosylated, human beta-
CC secretase polypeptide characterised by structural coordinates comprising
CC a root mean square deviation of conserved residue backbone atoms of less
CC than 1.5 Angstrom when superimposed on backbone atoms described by
CC structural coordinates. The crystal is useful for determining the three-
CC dimensional structure of beta-secretase and other related proteins. This
CC is the amino acid sequence of a mature human beta-secretase (BACE)
CC protein.
XX
SQ Sequence 408 AA;

Query Match 100.0%; Score 144; DB 8; Length 408;
Best Local Similarity 100.0%; Pred. No. 1.7e-13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYYVEMTVGSPPQTLNILVDTGSSNFAV 28
||||||||||||||||||||||||||||
Db 32 GYYVEMTVGSPPQTLNILVDTGSSNFAV 59

RESULT 7
ADI64640
ID ADI64640 standard; protein; 411 AA.
XX
AC ADI64640;
XX
DT 22-APR-2004 (first entry)
XX
DE Mature human beta-secretase (BACE) protein seq id 1.
XX
KW crystal; glycosylated human beta-secretase; BACE; human beta-secretase;
KW protein co-ordinate data.
XX
OS Homo sapiens.
XX
PN US2004014194-A1.
XX
PD 22-JAN-2004.
XX
PF 26-MAR-2003; 2003US-00400273.
XX
PR 27-MAR-2002; 2002US-0367937P.
XX
PA (SCHE) SCHERING CORP.
XX
PI Beyer BM, Hammond GS, Reichert P, Strickland C, Wang W, Weber PC;
PI Wong GT, Zhang L;
XX
DR WPI; 2004-167920/16.
XX
PT New crystal comprising a glycosylated, human beta-secretase polypeptide,
PT useful for determining the three-dimensional structure of beta-secretase
PT and other related proteins.
XX
PS Claim 5; SEQ ID NO 1; 107pp; English.
XX
CC The invention describes a crystal comprising a glycosylated, human beta-
CC secretase polypeptide characterised by structural coordinates comprising
CC a root mean square deviation of conserved residue backbone atoms of less
CC than 1.5 Angstrom when superimposed on backbone atoms described by
CC structural coordinates. The crystal is useful for determining the three-
CC dimensional structure of beta-secretase and other related proteins. This
CC is the amino acid sequence of a mature human beta-secretase (BACE)
CC protein.
XX
SQ Sequence 411 AA;

Query Match 100.0%; Score 144; DB 8; Length 411;
Best Local Similarity 100.0%; Pred. No. 1.7e-13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYYVEMTVGSPPQTLNILVDTGSSNFAV 28
||||||||||||||||||||||||||||
Db 29 GYYVEMTVGSPPQTLNILVDTGSSNFAV 56

RESULT 8
ADJ57790
ID ADJ57790 standard; protein; 411 AA.
XX
AC ADJ57790;
XX
DT 06-MAY-2004 (first entry)
XX
DE BACE WT R56KR57 protein.
XX
KW beta site APP cleaving enzyme; BACE; Nootropic; Neuroprotective;
KW Alzheimer's disease.
XX
OS Synthetic.
XX
PN WO2004011641-A2.
XX
PD 05-FEB-2004.
XX
PF 25-JUL-2003; 2003WO-GB003200.
XX
PR 26-JUL-2002; 2002US-0398681P.
XX
PA (ASTE-) ASTEX TECHNOLOGY LTD.
XX
PI Vuillard LMM, Patel SJ, Yon JR, Cleasby A, Hamilton BJ, Shah A;
XX
DR WPI; 2004-169242/16.
XX
PT New beta site APP cleaving enzyme (BACE) protein, useful for treating or
PT preventing Alzheimer's disease or Alzheimer's-type pathology of Down's
PT syndrome.
XX
PS Claim 10; SEQ ID NO 19; 145pp; English.
XX
CC The present invention relates to a beta site APP cleaving enzyme (BACE)
CC protein. The compound or the composition is useful in medicine and the
CC BACE crystal structure is useful for drug discovery. The BACE protein,
CC compounds, pharmaceutical compositions, medicament, drug or other
CC composition comprising the compound is useful for treating or preventing
CC Alzheimer's disease or Alzheimer's-type pathology of Down's syndrome. The
CC present sequence represents the DNA sequence for a BACE protein.
XX
SQ Sequence 411 AA;

Query Match 100.0%; Score 144; DB 8; Length 411;
Best Local Similarity 100.0%; Pred. No. 1.7e-13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYYVEMTVGSPPQTLNILVDTGSSNFAV 28
||||||||||||||||||||||||||||
Db 32 GYYVEMTVGSPPQTLNILVDTGSSNFAV 59

RESULT 9
ADJ57791
ID ADJ57791 standard; protein; 411 AA.
XX
AC ADJ57791;
XX
DT 06-MAY-2004 (first entry)
XX
DE BACE N-Q R56KR57noHis protein.
XX
KW beta site APP cleaving enzyme; BACE; Nootropic; Neuroprotective;
KW Alzheimer's disease.
XX

OS Synthetic.
XX
PN WO2004011641-A2.
XX
PD 05-FEB-2004.
XX
PF 25-JUL-2003; 2003WO-GB003200.
XX
PR 26-JUL-2002; 2002US-0398681P.
XX
PA (ASTE-) ASTEX TECHNOLOGY LTD.
XX
PI Vuillard LMM, Patel SJ, Yon JR, Cleasby A, Hamilton BJ, Shah A;
XX
DR WPI; 2004-169242/16.
XX
PT New beta site APP cleaving enzyme (BACE) protein, useful for treating or
PT preventing Alzheimer's disease or Alzheimer's-type pathology of Down's
PT syndrome.
XX
PS Claim 10; SEQ ID NO 20; 145pp; English.
XX
CC The present invention relates to a beta site APP cleaving enzyme (BACE)
CC protein. The compound or the composition is useful in medicine and the
CC BACE crystal structure is useful for drug discovery. The BACE protein,
CC compounds, pharmaceutical compositions, medicament, drug or other
CC composition comprising the compound is useful for treating or preventing
CC Alzheimer's disease or Alzheimer's-type pathology of Down's syndrome. The
CC present sequence represents the DNA sequence for a BACE protein.
XX
SQ Sequence 411 AA;

Query Match 100.0%; Score 144; DB 8; Length 411;
Best Local Similarity 100.0%; Pred. No. 1.7e-13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYYVEMTVGSPPQTLNILVDTGSSNFAV 28
||||||||||||||||||||||||||||
Db 32 GYYVEMTVGSPPQTLNILVDTGSSNFAV 59

RESULT 10
ABR61930
ID ABR61930 standard; protein; 414 AA.
XX
AC ABR61930;
XX
DT 12-SEP-2003 (first entry)
XX
DE Human promemapsin 2 protein fragment.
XX
KW Memapsin 1; nootropic; neuroprotective; memapsin 2; beta secretase;
KW beta-amyloid protein; Alzheimer's disease; promemapsin 2; human.
XX
OS Homo sapiens.
XX
PN WO2003039454-A2.
XX
PD 15-MAY-2003.
XX
PF 23-OCT-2002; 2002WO-US034324.
XX
PR 23-OCT-2001; 2001US-0335952P.
PR 27-NOV-2001; 2001US-0333545P.
PR 14-JAN-2002; 2002US-0348464P.
PR 14-JAN-2002; 2002US-0348615P.
PR 20-JUN-2002; 2002US-0390804P.
PR 19-JUL-2002; 2002US-0397557P.
PR 19-JUL-2002; 2002US-0397619P.
XX
PA (OKLA-) OKLAHOMA MEDICAL RES FOUND.
PA (UNII) UNIV ILLINOIS FOUND.
XX
PI Ghosh AK, Tang J, Bilcer G, Chang W, Hong L, Koelsch G, Loy J;
PI Turner RT;
XX
DR WPI; 2003-541410/51.
XX
PT New peptide compounds are memapsin beta secretase inhibitors used for
PT treating Alzheimer's disease.
XX
PS Example; Fig 12; 407pp; English.
XX
CC The invention relates to peptide compounds of specified formula. The
CC compounds exhibit memapsin 2-beta secretase inhibitory activity relative
CC to memapsin 1-beta secretase and reduce the accumulation of beta-amyloid
CC protein. The compounds can be used for treating Alzheimer's disease. The
CC present sequence represents a human promemapsin 2 protein fragment used
CC in crystal strictures
XX
SQ Sequence 414 AA;

Query Match 100.0%; Score 144; DB 6; Length 414;
Best Local Similarity 100.0%; Pred. No. 1.7e-13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYYVEMTVGSPPQTLNILVDTGSSNFAV 28
||||||||||||||||||||||||||||
Db 34 GYYVEMTVGSPPQTLNILVDTGSSNFAV 61

RESULT 11
ADC72735
ID ADC72735 standard; protein; 414 AA.
XX
AC ADC72735;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human beta-site aspartyl protease cleaving enzyme catalytic domain.
XX
KW neuroprotective; nootropic; crystalline; Beta-site APP cleaving enzyme;
KW BACE; aspartyl protease; Alzheimer's disease; protein co-ordinate data.
XX
OS Homo sapiens.
XX
PN WO2003012089-A2.
XX
PD 13-FEB-2003.
XX
PF 26-JUL-2002; 2002WO-GB003461.
XX
PR 26-JUL-2001; 2001US-0308366P.
XX
PA (ASTE-) ASTEX TECHNOLOGY LTD.
PA (JANC) JANSSEN PHARM NV.
XX
PI Yon J, Cleasby A, Bruinzeel WD, Masure SLJ, Tickle I, Sharff A;
XX
DR WPI; 2003-239524/23.
DR N-PSDB; ADC72736.
XX
PT New Beta-site APP cleaving enzyme (BACE) proteins and protein crystal,
PT useful in designing compounds that inhibit or modulate BACE, in drug
PT screening assays, and in identifying receptors.
XX
PS Disclosure; Fig 2A; 272pp; English.
XX
CC The invention relates to a new crystalline form of Beta-site APP cleaving
CC enzyme (BACE) or its functional portion having an active site containing
CC one or more ligands other than the natural substrate or the substrate
CC that occurs naturally or physiologically within the active site.
CC Inhibitors of BACE protein or its functional portion is useful for
CC preparing a composition or medicament for inhibiting BACE or the
CC production of A-beta or its fragments, and in therapy for treating
CC Alzheimer's disease. The BACE crystals and proteins may be used to design

```
CC   compounds that inhibit or modulate BACE, in drug screening assays, and in
CC   identifying receptors. This sequence represents a fragment of the full
CC   length BACE protein from amino acid 76 to the C-terminus.
XX
SQ   Sequence 414 AA;

  Query Match             100.0%;  Score 144;  DB 7;  Length 414;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-13;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GYYVEMTVGSPPQTLNILVDTGSSNFAV 28
              ||||||||||||||||||||||||||||
Db         29 GYYVEMTVGSPPQTLNILVDTGSSNFAV 56


RESULT 12
AAB07899
ID   AAB07899 standard; protein; 415 AA.
XX
AC   AAB07899;
XX
DT   14-NOV-2000  (first entry)
XX
DE   Amino acid sequence of a human beta-secretase enzyme fragment.
XX
KW   Beta-secretase; beta-amyloid precursor protein; beta-amyloid peptide;
KW   amyloid plaque component; Alzheimer's disease; amyloidogenic disease;
KW   inhibitor.
XX
OS   Homo sapiens.
XX
PN   WO200047618-A2.
XX
PD   17-AUG-2000.
XX
PF   10-FEB-2000; 2000WO-US003819.
XX
PR   10-FEB-1999;   99US-0119571P.
PR   15-JUN-1999;   99US-0139172P.
XX
PA   (ELAN-) ELAN PHARM INC.
XX
PI   Anderson JP,  Basi G,  Doane MT,  Frigon N,  John V,  Power M;
PI   Sinha S,  Tatsuno G,  Tung J,  Wang S,  Mcconlogue L;
XX
DR   WPI; 2000-533011/48.
XX
PT   Purified beta-secretase protein used in assays to discover inhibitors
PT   which can be used for the treatment of amyloidogenic diseases e.g.
PT   Alzheimer's disease.
XX
PS   Claim 10; Fig 3B; 121pp; English.
XX
CC   The specification describes a beta-secretase enzyme. The enzyme cleaves
CC   beta-amyloid precursor protein to produce beta-amyloid peptide. This
CC   enzyme is therefore implicated in the production of amyloid plaque
CC   components which accumulate in the brains of individuals afflicted with
CC   Alzheimer's disease. Inhibitors of beta-secretase are administered to a
CC   mammalian subject e.g. with Alzheimer's disease or Alzheimer's disease-
CC   like pathology to test if they maintain or improve cognitive ability or
CC   reduce the plaque burden. The compounds are used for the treatment of
CC   amyloidogenic diseases e.g. Alzheimer's disease. The present sequence
CC   represents a human beta-secretase enzyme fragment
XX
SQ   Sequence 415 AA;

  Query Match             100.0%;  Score 144;  DB 3;  Length 415;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-13;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GYYVEMTVGSPPQTLNILVDTGSSNFAV 28
              ||||||||||||||||||||||||||||
Db         29 GYYVEMTVGSPPQTLNILVDTGSSNFAV 56


RESULT 13
ADJ57792
ID   ADJ57792 standard; protein; 417 AA.
XX
AC   ADJ57792;
XX
DT   06-MAY-2004  (first entry)
XX
DE   BACE N-Q R56KR57 crystallised protein.
XX
KW   beta site APP cleaving enzyme; BACE; Nootropic; Neuroprotective;
KW   Alzheimer's disease.
XX
OS   Synthetic.
XX
PN   WO2004011641-A2.
XX
PD   05-FEB-2004.
XX
PF   25-JUL-2003; 2003WO-GB003200.
XX
PR   26-JUL-2002; 2002US-0398681P.
XX
PA   (ASTE-) ASTEX TECHNOLOGY LTD.
XX
PI   Vuillard LMM,  Patel SJ,  Yon JR,  Cleasby A,  Hamilton BJ,  Shah A;
XX
DR   WPI; 2004-169242/16.
XX
PT   New beta site APP cleaving enzyme (BACE) protein, useful for treating or
PT   preventing Alzheimer's disease or Alzheimer's-type pathology of Down's
PT   syndrome.
XX
PS   Claim 10; SEQ ID NO 21; 145pp; English.
XX
CC   The present invention relates to a beta site APP cleaving enzyme (BACE)
CC   protein. The compound or the composition is useful in medicine and the
CC   BACE crystal structure is useful for drug discovery. The BACE protein,
CC   compounds, pharmaceutical compositions, medicament, drug or other
CC   composition comprising the compound is useful for treating or preventing
CC   Alzheimer's disease or Alzheimer's-type pathology of Down's syndrome. The
CC   present sequence represents the DNA sequence for a BACE protein.
XX
SQ   Sequence 417 AA;

  Query Match             100.0%;  Score 144;  DB 8;  Length 417;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-13;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GYYVEMTVGSPPQTLNILVDTGSSNFAV 28
              ||||||||||||||||||||||||||||
Db         32 GYYVEMTVGSPPQTLNILVDTGSSNFAV 59


RESULT 14
AAY88437
ID   AAY88437 standard; protein; 425 AA.
XX
AC   AAY88437;
XX
DT   03-AUG-2000  (first entry)
XX
DE   Human Asp2 amino acid sequence containing proteolytic cleavage site.
XX
KW   Aspartyl protease; aspartase; amyloid precursor protein; APP; Asp 2;
KW   Alzheimer's disease; beta secretase site.
XX
OS   Homo sapiens.
XX
PN   WO200017369-A2.
XX
```

PD 30-MAR-2000.
XX
PF 23-SEP-1999; 99WO-US020881.
XX
PR 24-SEP-1998; 98US-0101594P.
XX
PA (PHAA) PHARMACIA & UPJOHN CO.
XX
PI Gurney ME, Bienkowski MJ, Heinrikson RL, Parodi LA, Yan R;
XX
DR WPI; 2000-303209/26.
DR N-PSDB; AAA15677.
XX
PT New enzyme designated human aspartase useful in research into Alzheimer's
PT Disease is capable of cleaving amyloid protein precursor at the beta
PT secretase site to produce amyloid beta peptide.
XX
PS Example 9; Page 166-168; 183pp; English.
XX
CC This sequence represents a modified version of the human aspartase 2
CC (Asp2) nucleotide sequence. The sequence is used in the bacterial
CC expression of human Asp2L. The invention relates to a protease (e.g.
CC Asp2) capable of cleaving the beta secretase site of amyloid precursor
CC protein (APP). The protease contains a sequence encoding the amino acid
CC sequence DTG and a sequence encoding DSG or DTG separated by 100-300
CC amino acids. When mutated the APP gene causes an autosomal dominant form
CC of Alzheimer's disease. APP localises to the cell surface membrane and
CC have a single C-terminal transmembrane domain. Proteolytic processing of
CC APP produces the amyloid beta protein, which is possibly very important
CC in Alzheimer's disease. The invention includes a nucleotide sequence
CC encoding the protease, a vector containing the nucleotide sequence, and a
CC cell line comprising the vector. Methods for screening for inhibitors of
CC beta secretase activity are also given in the invention. The human
CC aspartase protein and nucleotide sequences and the methods for
CC identifying inhibitors of the protease, are useful in the treatment of
CC and research in to Alzheimer's disease
XX
SQ Sequence 425 AA;

Query Match 100.0%; Score 144; DB 3; Length 425;
Best Local Similarity 100.0%; Pred. No. 1.8e-13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYYVEMTVGSPPQTLNILVDTGSSNFAV 28
||||||||||||||||||||||||||||
Db 46 GYYVEMTVGSPPQTLNILVDTGSSNFAV 73

RESULT 15
AAU07214
ID AAU07214 standard; protein; 425 AA.
XX
AC AAU07214;
XX
DT 11-SEP-2003 (revised)
DT 24-OCT-2001 (first entry)
XX
DE T7-caspase-caspase 8-human aspartyl protease 2a deltaTM.
XX
KW Human; aspartyl protease 1; Asp-1; nootropic; neuroprotective;
KW aspartyl protease 2; Asp2; amyloid protein precursor; APP;
KW beta-secretase; Alzheimer's disease.
XX
OS Homo sapiens.
OS Enterobacteria phage T7.
XX
PN WO200149097-A2.
XX
PD 12-JUL-2001.
XX
PF 09-MAY-2001; 2001WO-IB000797.
XX
PR 09-MAY-2001; 2001WO-IB000797.
XX
PA (BIEN/) BIENKOWSKI M J.
PA (GURN/) GURNEY M E.
PA (HEIN/) HEINRIKSON R L.
PA (PARO/) PARODI L A.
PA (YANR/) YAN R.
XX
PI Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;
XX
DR WPI; 2001-502548/55.
DR N-PSDB; AAS11714.
XX
PT Novel purified polypeptide comprising fragment of mammalian aspartyl
PT protease 2, lacking Asp2 transmembrane domain and retaining beta
PT secretase activity of Asp2 useful for identifying inhibitors of Asp2
PT activity.
XX
PS Example 9; Page 158-159; 185pp; English.
XX
CC The invention relates to a novel purified polypeptide comprising a
CC fragment of mammalian aspartyl protease 2 (Asp2) protein which lacks the
CC Asp2 transmembrane domain and the Asp2 protein, and where the polypeptide
CC and the fragment retain the beta-secretase activity of the mammalian Asp2
CC protein. Also included is an isoform of amyloid protein precursor (APP)
CC comprising the amino acid sequence of a APP or its fragment containing an
CC APP cleavage site recognisable by a mammalian beta-secretase, and further
CC comprising two lysine residues at the carboxyl terminus of the amino acid
CC sequence of the mammalian APP or APP fragment. The polypeptides are used
CC for assaying for modulators of beta-secretase activity; identifying
CC agents that inhibit the APP processing activity of human Asp2 aspartyl
CC protease (Hu-Asp2); identifying agents that modulate the activity of Asp2
CC ; and for reducing cellular production of amyloid beta (Abeta) from APP.
CC Agents identified by the above methods are useful for treating
CC Alzheimer's disease; and for identifying modulators of amyloid-beta
CC (Abeta) peptide production, for use in designing therapeutics for the
CC treatment or prevention of Alzheimer's disease. Probes and primers
CC derived from Asp nucleic acid sequences are useful for detecting Hu-Asp
CC nucleic acids in in vitro assays and in Northern and Southern blots. The
CC present sequence represents the amino acid sequence of T7-caspase-caspase
CC 8-human-Asp-2a delta TM construct which has a T7 tag, a caspase 8 leader
CC sequence and cleavage site, and lacks the transmembrane domain. This
CC construct was used for bacterial expression and purification of human
CC Asp2a. (Updated on 11-SEP-2003 to standardise OS field)
XX
SQ Sequence 425 AA;

Query Match 100.0%; Score 144; DB 4; Length 425;
Best Local Similarity 100.0%; Pred. No. 1.8e-13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYYVEMTVGSPPQTLNILVDTGSSNFAV 28
||||||||||||||||||||||||||||
Db 46 GYYVEMTVGSPPQTLNILVDTGSSNFAV 73

Search completed: July 26, 2005, 16:44:20
Job time : 166 secs